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RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
 RA Seebaghi S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,
 RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.,
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RL [6]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE:Ovary;
 RC MEDLINE:2238257; PubMed:12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diachenko L., Marulana K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalcron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Millar S.J.,
 RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield J.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RL [7]
 RN PROTEIN SEQUENCE OF 28-103 AND 123-130, AND N-GLYCOSYLATION.
 RP PubMed:764639;
 RA Naik U.P., Shrillich Y.H., Kornecki E.,
 RT "Mechanisms of platelet activation by a stimulatory antibody: cross-
 RT linking of a novel platelet receptor for monoclonal antibody F11 with
 RT the Fc gamma R1 receptor.";
 RL Biochem. J. 310:155-162(1995).
 RL [8]
 RN PROTEIN SEQUENCE OF 28-42.
 RP PubMed:15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RL [9]
 RN PROTEIN SEQUENCE OF 28-39.
 RP TISSUE:Platelet;
 RC MEDLINE:22608296; PubMed:12665801; DOI=10.1036/hdbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.,
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:565-569(2003).
 RL [10]
 RN INTERACTION WITH MPDZ.
 RP PubMed:11489913; DOI=10.1083/jcb.200103047;
 RA Itoh M., Sasaki H., Furuse M., Ozaki H., Kita T., Tsukita S.,
 RT "Junctional adhesion molecule (JAM) binds to PAR-3: a possible
 RT mechanism for the recruitment of PAR-3 to tight junctions.";
 RL J. Cell Biol. 154:491-497(2001).
 RL [11]
 RN REVIEW, AND NOMENCLATURE.
 RP PubMed:12810109; DOI=10.1016/S1471-4906(03)00117-0;
 RA Miller W.A.,
 RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
 RT and the inflammatory response.";
 RL Trends Immunol. 24:327-334(2003).
 RL -1- FUNCTION: Seems to plays a role in epithelial tight junction

formation. Appears early in primordial forms of cell junctions and
 recruits PAR3. The association of the PAR6-PAR3 complex may
 prevent the interaction of PAR3 with JAM1, thereby preventing
 tight junction assembly (By similarity). Plays a role in
 regulating monocyte transmigration involved in integrity of
 epithelial barrier. Involved in platelet activation.
 -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 association between PAR3 and PAR6 probably disrupts this
 interaction (By similarity). Interacts with the ninth PDZ domain
 of MPDZ.
 -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 localized at tight junctions of both epithelial and endothelial
 cells.
 -1- PTM: N-Glycosylated.
 -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
 -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
 domain.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AF111713; RAD4050.1; -; mRNA.
 CC EMBL: AF207907; AAF2829.1; -; mRNA.
 CC EMBL: AF172398; AAD4877.1; -; mRNA.
 CC EMBL: AL136649; CAB6584.1; -; mRNA.
 CC EMBL: AY358966; AAO89255.1; -; mRNA.
 CC EMBL: BC001533; AAH01533.1; -; mRNA.
 CC PIR: A59406; S56749.
 CC PDB: 1NEQ; X-ray; A/b=27-233.
 CC Ensembl: ENSG00000158769; Homo sapiens.
 CC HGNC: HGNC:14685; F1LR.
 CC MIM: 605721; -.
 CC GO: GO:0005911; C:intercellular junction; TAS.
 CC GO: GO:006954; P:inflammatory response; TAS.
 CC InterPro: IPR007110; Ig-like.
 CC Pfam: PF00047; Ig_1.
 CC PROSITE: PS50835; IG_LIKE; 2.
 CC 3D-structure; Direct protein sequencing; Glycoprotein;
 CC Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
 CC STGMN 1 27
 CC CHAIN 28 299
 CC TOPO_DOM 28 238
 CC TRANSMEM 239 259
 CC TOPO_DOM 260 299
 CC DOMAIN 28 125
 CC DOMAIN 135 228
 CC CARBOHYD 185 185
 CC DISULFID 50 109
 CC DISULFID 153 212
 CC SEQUENCE 299 AA; 23583 MW; D95DE2FEA23D2851 CRC64;
 Query Match 100.0%; Score 1544; DB 1; Length 299;
 Best Local Similarity 100.0%; Pred. No. 1,8e-111;
 Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTAQVERKLCIFILAILLCSIALGVSIVHSSEPRVIRIPENNVPLKSCAYSGFSSPRV 60
 DB 1 MGTAQVERKLCIFILAILLCSIALGVSIVHSSEPRVIRIPENNVPLKSCAYSGFSSPRV 60
 QY 61 EWFQDGDTRLVLCYNNKNTASJEDRTPLPTGTPFSVTRDGTTCWVSESGNSYG 120
 DB 61 EWFQDGDTRLVLCYNNKNTASJEDRTPLPTGTPFSVTRDGTTCWVSESGNSYG 120
 QY 61 EWFQDGDTRLVLCYNNKNTASJEDRTPLPTGTPFSVTRDGTTCWVSESGNSYG 120
 DB 61 EWFQDGDTRLVLCYNNKNTASJEDRTPLPTGTPFSVTRDGTTCWVSESGNSYG 120
 QY 121 EVKFKLVLPSPSPATINISSATIGRAVLTCSEBQSPSPSEXTWFKDGIWMTNPKST 180
 DB 121 EVKFKLVLPSPSPATINISSATIGRAVLTCSEBQSPSPSEXTWFKDGIWMTNPKST 180
 QY 121 EVKFKLVLPSPSPATINISSATIGRAVLTCSEBQSPSPSEXTWFKDGIWMTNPKST 180
 DB 121 EVKFKLVLPSPSPATINISSATIGRAVLTCSEBQSPSPSEXTWFKDGIWMTNPKST 180
 QY 181 RAFSNSSVYINPTTGLVFPDPLASDTEGYSCEARNGYGPMTSNAYRMAVEENVGVIV 240
 DB 181 RAFSNSSVYINPTTGLVFPDPLASDTEGYSCEARNGYGPMTSNAYRMAVEENVGVIV 240
 QY 181 RAFSNSSVYINPTTGLVFPDPLASDTEGYSCEARNGYGPMTSNAYRMAVEENVGVIV 240
 DB 181 RAFSNSSVYINPTTGLVFPDPLASDTEGYSCEARNGYGPMTSNAYRMAVEENVGVIV 240

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241 AAVVTLILGILVFGIMFAYSRGHPDRTKGGTSSKKVYISQPSARSGEFPKOTSSFLV 299
 241 AAVVTLILGILVFGIMFAYSRGHPDRTKGGTSSKKVYISQPSARSGEFPKOTSSFLV 299

14 HUMAN
 O6F1B4_HUMAN PRELIMINARY; PRT; 299 AA.
 O6F1B4;

05-JUL-2004 (TREMBLrel. 27, Created)
 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 P1LR protein (P1 receptor protein) (JAMI) (Hypothetical protein
 P1LR06711).

Name=P1LR, ORNames=Rp11-544M22-2.001;
 Homo sapiens (Human).
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 Homo.

NCBI_TaxId=9606;

[1]

NUCLEOTIDE SEQUENCE.
 Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

[2]

NUCLEOTIDE SEQUENCE.
 MEDLINE=20537956; PubMed=11087121; DOI=10.1080/15216540050176593;
 Gupta S.K., Pillarsetti K., Ohlstein B.H.;
 "Platelet agonist P1 receptor is a member of the immunoglobulin
 superfamily and identical with junctional adhesion molecule (JAM):
 regulation of expression in human endothelial cells and macrophages."
 JMBB Life 50:51-56(2000).

[3]

NUCLEOTIDE SEQUENCE.
 MEDLINE=22701983; PubMed=12817473; DOI=10.1515/BC.2003.085;
 Menzel K., Felix S.B., Plachmeier C., Heere P., Schulze W.,
 Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.,
 Hoehe M.R.;
 "Identification and characterization of KAT, a novel gene
 preferentially expressed in several human cancer cell lines."
 Biol. Chem. 384:763-775(2003).

[4]

NUCLEOTIDE SEQUENCE.
 TRS5B2-Placenta;
 Oseuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J.,
 Makamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,
 Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,
 Kotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
 Isegaki T.;
 "Signal Sequence and Keyword Trap in silico for Selection of Full-
 length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
 tagged cDNA Libraries."
 DNA Res. 12:117-126(2005).

[5]

NUCLEOTIDE SEQUENCE.
 Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 Shellan M., Farmer A.;
 "Cloning of human full-length cDNAs in BD Creator(TM) System donor
 vector";
 Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

[6]

NUCLEOTIDE SEQUENCE.
 Harrison B.;
 Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 EMBL; CR53512; CAG38543.1; -; mRNA.
 EMBL; AF191495; AAG28379.1; -; mRNA.
 EMBL; AF490407; AA084556.1; -; Genomic DNA.
 EMBL; BT020103; AAV38906.1; -; mRNA.
 EMBL; AL591806; CA115365.1; -; Genomic DNA.
 EMBL; AK075152; BAC11436.1; -; mRNA.
 EMBL; O6F1B4; 25-233.

DR Ensembl: ENSG00000158769; Homo sapiens.
 DR GO: 0004872; P: receptor activity; IEA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_1like; 2.
 KW Receptor.
 SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 100.0%; Score 1544; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 1.8e-111;
 Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAAQVRKRLCLPILAILLCSIALGSVTHSSSEPRVIRBNPVKLSCAVSGFSSPRV 60
 DB 1 MGTAAQVRKRLCLPILAILLCSIALGSVTHSSSEPRVIRBNPVKLSCAVSGFSSPRV 60
 QY 61 EMKFDQDPTRLVCNNKKTASYEDRYTFLPTGTFPSVTRBDGYTCWVSBEGNSYG 120
 DB 61 EMKFDQDPTRLVCNNKKTASYEDRYTFLPTGTFPSVTRBDGYTCWVSBEGNSYG 120
 QY 121 EVKVKILVLPSPKPTVNPSSATIGNRAVLTCSEODGSPSEYTFWPDGIVMPTNPKST 180
 DB 121 EVKVKILVLPSPKPTVNPSSATIGNRAVLTCSEODGSPSEYTFWPDGIVMPTNPKST 180
 QY 181 RAFNSSTVNLPTGELVFPDPLASDPTGEYSCEARNVGTPTMSNAYMEVENVGVIV 240
 DB 181 RAFNSSTVNLPTGELVFPDPLASDPTGEYSCEARNVGTPTMSNAYMEVENVGVIV 240
 QY 241 AAVVTLILGILVFGIMFAYSRGHPDRTKGGTSSKKVYISQPSARSGEFPKOTSSFLV 299
 DB 241 AAVVTLILGILVFGIMFAYSRGHPDRTKGGTSSKKVYISQPSARSGEFPKOTSSFLV 299

RESULT 3

Q9YSB2 HUMAN
 ID Q9YSB2_HUMAN PRELIMINARY; PRT; 299 AA.
 AC Q9YSB2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Junction adhesion molecule.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 CX NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Liu Y., Nussat A., Schneel F.J., Walsh S., Reeves T.A., Pochet M.,
 Foley C., Parks C.A.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 DR EMBL; AF154005; AAD43794.1; -; mRNA.
 DR HSP; Q9Y624; INBO.
 DR SMK; Q9YSB2; 20-193.
 DR Ensembl: ENSG00000158769; Homo sapiens.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG_1like; 1.
 KW Immunoglobulin domain; Transmembrane.
 SQ SEQUENCE 299 AA; 28122 MW; FE38521A911582D0 CRC64;

Query Match 83.0%; Score 1281; DB 2; Length 299;
 Best Local Similarity 86.0%; Pred. No. 3.8e-91;
 Matches 257; Conservative 0; Mismatches 2; Indels 40; Gaps 2;

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 07:02:51 ; Search time 229 Seconds

(without alignments)
921.192 Million cell updates/sec

Title: US-10-785-433-1

Perfect score: 1544

Sequence: 1 MGRIKQVERKLLCLFILAIL.....YSPSARSEGEFKQTSSFLV 299

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1544	100.0	299	1 JAMI_HUMAN	Q9Y624 homo sapien
2	1544	100.0	299	2 Q6FI54_HUMAN	Q6FI54 homo sapien
3	1281	83.0	259	2 Q9Y5B2_HUMAN	Q9Y5B2 homo sapien
4	1176.5	76.2	298	1 JAMI_BOVIN	Q9Y556 bos taurus
5	1176.5	76.2	298	2 Q5E9V8_BOVIN	Q5E9V8 bos taurus
6	1096.5	71.0	300	1 JAMI_RAT	Q9JHY1 rattus norv
7	1079.5	69.9	300	2 Q8VC39_MOUSE	Q8VC39 mus musculu
8	1073.5	69.5	300	1 JAMI_MOUSE	Q86792 mus musculu
9	700	45.3	173	2 Q9JKD5_RAT	Q9JKD5 rattus norv
10	602.5	39.0	289	2 Q7ZK05_XENLA	Q7ZK05 xenopus lae
11	580.5	37.6	296	2 Q640C0_XENLA	Q640C0 xenopus lae
12	580.5	37.6	300	2 Q7SYO7_XENLA	Q7SYO7 xenopus lae
13	571.5	37.0	292	2 Q66172_BRARE	Q66172 brachydanio
14	560.5	36.3	291	2 Q66J15_XENTR	Q66J15 xenopus tro
15	534.5	34.6	260	2 Q4S8Z8_TETNG	Q4S8Z8 tetradon n
16	424	27.9	298	1 JAMI_HUMAN	P57087 homo sapien
17	424	27.5	310	1 JAMI_HUMAN	Q9HX67 homo sapien
18	411	26.6	310	1 JAMI_MOUSE	Q948B7 mus musculu
19	410	26.6	298	1 JAMI_MOUSE	Q9J159 mus musculu
20	403	26.1	310	1 JAMI_RAT	Q661F2 rattus norv
21	360.5	23.3	243	2 Q5ZJ01_CHICK	Q5ZJ01 gallus gall
22	338	21.9	257	2 Q4SOM3_TETNG	Q4SOM3 tetradon n
23	293	19.0	273	2 Q4RRS6_TETNG	Q4RRS6 tetradon n
24	280.5	18.2	319	1 G9A33_MOUSE	Q9JKA5 mus musculu
25	272.5	17.6	319	1 G9A33_MOUSE	Q9J795 homo sapien
26	272.5	17.6	319	2 Q5VZP6_HUMAN	Q5VZP6 homo sapien
27	257.5	16.7	344	2 Q568F7_BRARE	Q568F7 brachydanio
28	232	15.0	327	1 VSIG2_HUMAN	Q961Q7 homo sapien
29	231.5	15.0	328	1 VSIG2_HUMAN	Q9J109 mus musculu
30	220	14.2	335	2 Q9PMR4_CHICK	Q9PMR4 gallus gall
31	219	14.2	335	2 Q9YGH1_CHICK	Q9YGH1 gallus gall

32	216	14.0	283	2 Q4V7Q4_XENLA	Q4V7Q4 xenopus lae
33	214.5	13.9	2673	2 Q96SC3_HUMAN	Q96SC3 homo sapien
34	213.5	13.8	5635	2 Q5YR7_HUMAN	Q5YR7 homo sapien
35	213.5	13.8	5636	2 Q96RW7_HUMAN	Q96RW7 homo sapien
36	212	13.7	335	2 Q9YGV5_CHICK	Q9YGV5 gallus gall
37	210.5	13.6	372	1 CXAR_BRARE	Q9Y550 brachydanio
38	210	13.6	332	2 Q6P359_XENTR	Q6P359 xenopus tro
39	208.5	13.5	318	2 Q91664_XENLA	Q91664 xenopus lae
40	208.5	13.5	428	2 Q5U2P2_RAT	Q5U2P2 rattus norv
41	207.5	13.4	365	1 CXAR_HUMAN	P78310 homo sapien
42	207.5	13.4	365	1 CXAR_PONPY	Q52764 pongo pygma
43	207.5	13.4	431	2 Q5DUX1_HUMAN	Q5DUX1 homo sapien
44	205.5	13.3	414	2 Q5VU13_HUMAN	Q5VU13 homo sapien
45	204	13.2	529	2 Q4SMH3_TETNG	Q4SMH3 tetradon n
46	202	13.1	5533	2 Q5R1P6_BRARE	Q5R1P6 brachydanio
47	201.5	13.1	316	2 Q8VE98_MOUSE	Q8VE98 mus musculu
48	201	13.0	387	2 Q86XK7_HUMAN	Q86XK7 homo sapien
49	201	13.0	412	2 Q6M2S4_HUMAN	Q6M2S4 homo sapien
50	200	13.0	319	2 Q9TUB0_CANFA	Q9TUB0 canis famli
51	199	12.9	347	2 Q5XG64_XENTR	Q5XG64 xenopus tro
52	198.5	12.9	210	2 Q4RTW7_MACFA	Q4RTW7 macaca fasc
53	198	12.8	335	2 Q588B2_XENLA	Q588B2 xenopus lae
54	197	12.8	316	2 Q7TPB4_RAT	Q7TPB4 rattus norv
55	196	12.7	319	2 Q9TUV9_PIG	Q9TUV9 sus scrofa
56	196	12.7	365	1 CXAR_BOVIN	Q8WNV3 bos taurus
57	196	12.7	373	2 Q9H6B4_HUMAN	Q9H6B4 homo sapien
58	195	12.6	430	2 Q8N4F1_HUMAN	Q8N4F1 homo sapien
59	193	12.5	373	2 Q8R373_MOUSE	Q8R373 mus musculu
60	193	12.5	2528	2 Q4S2G3_TETNG	Q4S2G3 tetradon n
61	193	12.5	3493	2 Q4RJ20_TETNG	Q4RJ20 tetradon n
62	192.5	12.5	3198	2 Q9UG68_MANSE	Q9UG68 manduca sex
63	192.5	12.5	34350	2 Q8W242_HUMAN	Q8W242 homo sapien
64	192	12.4	365	1 CXAR_RAT	Q9T066 rattus norv
65	191.5	12.4	332	2 Q640U3_XENTR	Q640U3 xenopus tro
66	191	12.4	332	2 Q8ND02_HUMAN	Q8ND02 homo sapien
67	189.5	12.3	7962	2 Q10465_HUMAN	Q10465 homo sapien
68	189	12.2	365	1 CXAR_MOUSE	P97792 mus musculu
69	189	12.2	373	2 Q920S5_MOUSE	Q920S5 mus musculu
70	186	12.0	372	2 Q8K1G0_RAT	Q8K1G0 rattus norv
71	185.5	12.0	858	2 Q18466_HIRME	Q18466 hirtudo medl
72	185.5	12.0	1730	2 Q7YRQ7_PIG	Q7YRQ7 sus scrofa
73	185.5	12.0	3950	2 Q7YRFS_CANFA	Q7YRFS canis famli
74	183	11.9	434	2 Q4RF60_TETNG	Q4RF60 tetradon n
75	182	11.8	329	2 Q8N225_HUMAN	Q8N225 homo sapien
76	182	11.8	538	2 Q29123_PIG	Q29123 sus scrofa
77	182	11.8	1340	2 Q8ND42_HUMAN	Q8ND42 homo sapien
78	181.5	11.8	302	2 Q4T321_TETNG	Q4T321 tetradon n
79	181.5	11.8	862	1 CD22_MOUSE	P35329 mus musculu
80	181.5	11.8	1154	2 Q4SR72_TETNG	Q4SR72 tetradon n
81	181	11.7	390	1 ESAM_MACFA	Q95K13 macaca fasc
82	181	11.7	1093	1 LRIG1_HUMAN	Q96J41 homo sapien
83	181	11.7	1093	2 Q5XWD3_HUMAN	Q5XWD3 homo sapien
84	180.5	11.7	316	2 Q6UX12_HUMAN	Q6UX12 homo sapien
85	180.5	11.7	2016	2 Q86B07_DROME	Q86B07 drosophila
86	180.5	11.7	2224	2 Q9UIM1_DROME	Q9UIM1 drosophila
87	180	11.7	1296	2 Q7QJ29_ANOGA	Q7QJ29 anopheles g
88	179.5	11.6	388	2 Q91665_XENLA	Q91665 xenopus lae
89	179	11.6	534	2 Q8NC34_HUMAN	Q8NC34 homo sapien
90	179	11.6	534	2 Q8NB18_HUMAN	Q8NB18 homo sapien
91	179	11.6	534	2 Q5ZPR3_HUMAN	Q5ZPR3 mus sapien
92	179	11.6	538	2 Q28939_PIG	Q28939 sus scrofa
93	179	11.6	1048	2 Q7QH02_ANOGA	Q7QH02 anopheles g
94	178.5	11.6	316	2 Q9BXR1_HUMAN	Q9BXR1 homo sapien
95	178.5	11.6	399	1 VSIG4_HUMAN	Q9Y279 homo sapien
96	178.5	11.6	595	2 Q6ZRS5_HUMAN	Q6ZRS5 homo sapien
97	178.5	11.6	722	2 Q4KMG2_HUMAN	Q4KMG2 homo sapien
98	178.5	11.6	779	2 Q97136_MANSE	Q97136 manduca sex
99	178.5	11.6	837	2 Q97137_MANSE	Q97137 manduca sex
100	178.5	11.6	1252	2 Q96DN3_HUMAN	Q96DN3 homo sapien
101	178.5	11.6	1496	2 Q92626_HUMAN	Q92626 homo sapien
102	178	11.5	512	2 Q96DN8_HUMAN	Q96DN8 homo sapien
103	177.5	11.5	847	1 CD22_HUMAN	P20273 homo sapien
104	177.5	11.5	1269	2 Q01632_CABEL	Q01632 caenorhabdi

105	177.5	11.5	1273	2	044928 CAEEL	044928 caenorhabdi	178	166.5	10.8	394	1	ESAM MOUSE	Q925F2 mus musculus
106	176.5	11.4	533	2	08NCB6 HUMAN	08ncb6 homo sapien	179	166.5	10.8	622	2	Q9R0G6 MOUSE	Q9R0G6 mus musculus
107	176	11.4	390	1	ESAM HUMAN	Q9cap7 homo sapien	180	166.5	10.8	650	2	Q99XG6 MOUSE	Q99XG6 mus musculus
108	175.5	11.4	319	2	Q7OLK4 ANOGA	Q7olk4 anopheles g	181	166.5	10.8	1038	2	Q4TKB8 TETNG	Q4tkb8 tetradodon n
109	175.5	11.4	407	2	Q9D2J4 MOUSE	Q9d2j4 mus musculus	182	166	10.8	377	2	Q4RZV7 TETNG	Q4rzv7 tetradodon n
110	175.5	11.4	10495	2	Q4R922 TETNG	Q4r922 tetradodon n	183	166	10.8	563	2	Q5FWR8 XENTR	Q5fwr8 xenopus tro
111	175	11.3	882	2	Q4RVZ3 TETNG	Q4rvz3 tetradodon n	184	166	10.8	584	2	Q9Y3Y8 HUMAN	Q9y3y8 homo sapien
112	174.5	11.3	1725	2	Q7Q9I6 ANOGA	Q7q9i6 anopheles n	185	166	10.8	591	2	Q6NP04 DROME	Q6np04 drosophila
113	174	11.3	398	2	Q8N126 HUMAN	Q8n126 homo sapien	186	166	10.8	2772	2	Q9YAV4 DROME	Q9yav4 drosophila
114	174	11.3	413	2	Q64OR3 MOUSE	Q64or3 mus musculus	187	166	10.8	2894	2	Q7KRX2 DROME	Q7kxr2 drosophila
115	174	11.3	432	2	Q9UJP1 HUMAN	Q9ujp1 homo sapien	188	166	10.8	5175	2	Q8I0L3 CAEEL	Q8i0l3 caenorhabdi
116	174	11.3	2293	2	Q4TIM4 TETNG	Q4tim4 tetradodon n	189	166	10.8	5198	2	Q765I8 CAEEL	Q765i8 caenorhabdi
117	173.5	11.2	439	2	Q6RMT6 BOVIN	Q6rmt6 bos taurus	190	165.5	10.7	1164	2	Q66NMS DROYI	Q66nms drosophila
118	173.5	11.2	1268	2	Q6I9I9 CAEER	Q6i9i9 caenorhabdi	191	165.5	10.7	1389	2	Q90Z69 BRARE	Q90z69 brachydanio
119	173.5	11.2	1395	2	Q7KVK3 DROME	Q7kvk3 drosophila	192	165.5	10.7	1419	2	Q98SW3 BRARE	Q98sw3 brachydanio
120	173.5	11.2	1395	2	Q44924 DROME	Q44924 drosophila	193	165.5	10.7	2016	2	Q9NBN1 DROME	Q9nbn1 drosophila
121	173.5	11.2	1429	2	Q9W2I3 DROME	Q9w2i3 drosophila	194	165.5	10.7	4162	2	Q989I8 CHICK	Q989i8 gallus gall
122	173	11.2	300	2	Q7PV30 ANOGA	Q7pv30 anopheles g	195	165	10.7	344	1	CEAM6 HUMAN	P40199 homo sapien
123	173	11.2	367	2	Q6ZWL4 HUMAN	Q6zwl4 homo sapien	196	165	10.7	344	2	Q53XP7 HUMAN	Q53xp7 homo sapien
124	173	11.2	416	2	Q8N7I3 HUMAN	Q8n7i3 homo sapien	197	165	10.7	344	2	Q13774 HUMAN	Q13774 homo sapien
125	173	11.2	416	2	Q87IP8 HUMAN	Q87ip8 homo sapien	198	165	10.7	624	2	Q9ES66 RAT	Q9es66 ratius norv
126	173	11.2	1709	1	SN HUMAN	Q9bz22 homo sapien	199	165	10.7	5992	2	Q5W6I5 CAEEL	Q5w6i5 caenorhabdi
127	172.5	11.2	418	2	Q5O1T5 BRARE	Q5o1t5 brachydanio	200	165	10.7	6632	1	UNC89 CAEEL	Q01761 caenorhabdi
128	172.5	11.2	1227	2	Q2I038 CAEEL	Q2i038 caenorhabdi	201	165	10.7	7122	2	Q5W6I6 CAEEL	Q5w6i6 caenorhabdi
129	172.5	11.2	1431	2	Q8U060 MOUSE	Q8u060 mus musculus	202	165	10.7	7441	2	Q5W6I7 CAEEL	Q5w6i7 caenorhabdi
130	172	11.1	399	2	Q8N772 HUMAN	Q8n772 homo sapien	203	165	10.7	8081	2	Q72I20 CAEEL	Q72i20 caenorhabdi
131	172	11.1	602	2	Q86Y09 HUMAN	Q86y09 homo sapien	204	164.5	10.7	432	2	Q6RMT5 BOVIN	Q6rmt5 bos taurus
132	172	11.1	650	2	Q8NAB4 HUMAN	Q8nab4 homo sapien	205	164.5	10.7	739	1	VCAM1 CANFA	Q828260 canis famli
133	172	11.1	2597	2	Q6WRH9 RAT	Q6wrh9 rattus norv	206	164.5	10.7	765	2	Q9BKQ1 APICA	Q9bkq0 aplysia cal
134	172	11.1	2623	2	Q6MRIO HUMAN	Q6mr10 homo sapien	207	164.5	10.7	812	2	Q9BKQ0 APICA	Q9bkq0 aplysia cal
135	171.5	11.1	1693	2	Q4S6A5 TETNG	Q4s6a5 tetradodon n	208	164.5	10.7	1095	2	Q58EP4 BRARE	Q58ep4 brachydanio
136	171	11.1	324	2	Q7TMH2 MOUSE	Q7tmh2 mus musculus	209	164.5	10.7	1109	2	Q6PSH3 MOUSE	Q6psh3 mus musculus
137	171	11.1	343	2	Q8R4Y0 MOUSE	Q8r4y0 mus musculus	210	164.5	10.7	2016	2	Q8MKK6 DROME	Q8mkk6 drosophila
138	171	11.1	1091	1	LRIG3 HUMAN	P70193 mus musculus	211	164.5	10.7	2019	2	Q8MKK7 DROME	Q8mkk7 drosophila
139	171	11.1	1119	1	LRIG3 HUMAN	Q6uxm1 homo sapien	212	164.5	10.7	2019	2	Q8MKK8 DROME	Q8mkk8 anopheles g
140	170.5	11.0	375	2	Q6RMT4 BOVIN	Q6rmt4 bos taurus	213	164	10.6	595	2	Q7Q3K8 ANOGA	Q7q3k8 anopheles g
141	170.5	11.0	436	2	Q6VAN8 BOVIN	Q6van8 bos taurus	214	164	10.6	605	2	Q6GNL9 XENLA	Q6gnl9 xenopus lae
142	170.5	11.0	2013	2	Q8VHZ8 RAT	Q8vhz8 rattus norv	215	164	10.6	2222	2	Q4RY92 TETNG	Q4ry92 tetradodon n
143	170.5	11.0	453	2	Q9ERC8 MOUSE	Q9erc8 mus musculus	216	163.5	10.6	305	2	Q6P3A4 MOUSE	Q6p3a4 mus musculus
144	170	11.0	453	2	Q4T6S3 TETNG	Q4t6s3 tetradodon n	217	163.5	10.6	422	2	Q50Z49 BRARE	Q50z49 brachydanio
145	170	11.0	595	2	Q5W431 FUGRU	Q5w431 fugu rubrip	218	163.5	10.6	1020	2	Q8NHN0 HUMAN	Q8nhn0 homo sapien
146	170	11.0	630	2	Q5W436 FUGRU	Q5w436 fugu rubrip	219	163.5	10.6	1083	2	Q766F8 CAEEL	Q766f8 caenorhabdi
147	170	11.0	648	2	Q5W435 FUGRU	Q5w435 fugu rubrip	220	163.5	10.6	2022	2	Q7KQO5 DROME	Q7kqo5 drosophila
148	170	11.0	1117	1	LRIG3 MOUSE	Q6l1c6 mus musculus	221	163.5	10.6	249	2	Q5VST9 HUMAN	Q5vst9 homo sapien
149	170	11.0	1460	2	Q5HZ6I XENTR	Q5hz6i xenopus tro	222	163	10.6	249	2	Q58DG9 BOVIN	Q58dg9 bos taurus
150	169.5	11.0	452	2	Q4RRTO TETNG	Q4rrto tetradodon n	223	163	10.6	335	2	Q5XRA0 XENLA	Q5xra0 xenopus lae
151	169.5	11.0	753	2	Q5J7D9 MOUSE	Q5j7d9 mus musculus	224	163	10.6	520	2	Q9Z5P2 MOUSE	Q9z5p2 mus musculus
152	169.5	11.0	765	2	Q9TMA4 APICA	Q9tma4 aplysia cal	225	162.5	10.5	622	2	Q9ES55 MOUSE	Q9es55 mus musculus
153	169.5	11.0	799	2	Q8C3V5 MOUSE	Q8c3v5 mus musculus	226	162.5	10.5	622	2	Q9JKB2 MOUSE	Q9jkb2 mus musculus
154	169.5	11.0	799	2	Q8CIB8 MOUSE	Q8cib8 mus musculus	227	162.5	10.5	779	2	Q4STG7 TETNG	Q4stg7 tetradodon n
155	169.5	11.0	812	2	Q9TMA5 APICA	Q9tma5 aplysia cal	228	162.5	10.5	931	2	Q6KAM5 MOUSE	Q6kam5 mus musculus
156	169.5	11.0	881	2	Q4ROR3 TETNG	Q4rqr3 tetradodon n	229	162.5	10.5	1102	2	Q9Z3W7 MOUSE	Q9z3w7 mus musculus
157	169.5	11.0	932	2	Q9TMA6 APICA	Q9tma6 aplysia cal	230	162.5	10.5	1109	2	Q8CEB1 MOUSE	Q8ceb1 mus musculus
158	169.5	11.0	932	2	Q9BKX9 APICA	Q9bkx9 aplysia cal	231	162.5	10.5	1109	2	Q6AAZB0 MOUSE	Q6aazb0 mus musculus
159	169.5	11.0	1450	2	Q4SCTR TETNG	Q4sctr tetradodon n	232	162.5	10.5	1110	2	Q8CE73 MOUSE	Q8ce73 mus musculus
160	169.5	11.0	2222	2	Q9J394 DROME	Q9j394 drosophila	233	162	10.5	394	2	ESAM RAT	Q6ay44 rattus norv
161	169	10.9	343	2	Q8BY84 MOUSE	Q8by84 mus musculus	234	162	10.5	699	2	Q6IVL1 CAEER	Q6ivl1 caenorhabdi
162	169	10.9	396	2	Q99N28 MOUSE	Q99n28 m. nectin-11	235	162	10.5	795	2	Q90YMO BRARE	Q90ym0 brachydanio
163	169	10.9	739	1	VCAM1 MOUSE	P29533 mus musculus	236	162	10.5	862	2	Q4SST3 TETNG	Q4sst3 tetradodon n
164	169	10.9	739	2	Q9IX98 MOUSE	Q9ix98 mus musculus	237	162	10.5	1090	2	Q4TAD5 TETNG	Q4taad5 tetradodon n
165	169	10.9	739	2	Q8K0X1 MOUSE	Q8k0x1 mus musculus	238	162	10.5	1244	2	Q69YJ3 HUMAN	Q69yj3 homo sapien
166	169	10.9	1134	2	Q7I805 BRARE	Q7i805 brachydanio	239	161.5	10.5	429	2	Q6VAN7 BOVIN	Q6van7 bos taurus
167	169	10.9	2828	2	Q9NR39 HUMAN	Q9nr39 homo sapien	240	161.5	10.5	1048	2	Q7QHO1 ANOGA	Q7qho1 anopheles g
168	168.5	10.9	432	2	Q6DDE7 XENLA	Q6dde7 xenopus lae	241	161.5	10.5	2174	2	Q9QGOR DROME	Q9qgor drosophila
169	168.5	10.9	660	2	Q60926 HUMAN	Q60926 homo sapien	242	161	10.4	493	2	Q6PSY4 HUMAN	Q6psy4 homo sapien
170	168.5	10.9	3410	2	Q7TNO0 RAT	Q7tno0 rattus norv	243	161	10.4	650	2	Q9GKR2 BOVIN	Q9gkr2 bos taurus
171	168.5	10.9	6620	2	Q96AA2 HUMAN	Q96aa2 homo sapien	244	161	10.4	735	2	Q4RZ69 TETNG	Q4rz69 tetradodon n
172	167.5	10.8	372	2	Q6VAN6 BOVIN	Q6van6 bos taurus	245	161	10.4	739	2	Q9GKR3 BOVIN	Q9gkr3 bos taurus
173	167.5	10.8	1746	2	Q8WY19 HUMAN	Q8wy19 homo sapien	246	160.5	10.4	190	2	Q4SAI1 TETNG	Q4sai1 tetradodon n
174	167.5	10.8	2012	1	DSGAM HUMAN	Q6q465 homo sapien	247	160.5	10.4	368	2	Q6RMT3 BOVIN	Q6rmt3 bos taurus
175	167.5	10.8	2023	1	Q59GH3 HUMAN	Q59gh3 homo sapien	248	160.5	10.4	4071	2	Q6KDW1 CHICK	Q6kdw1 gallus gall
176	167	10.8	237	2	Q6DQX5 RABIT	Q6dqx5 oryctolagus	249	160	10.4	448	2	Q8IG45 DROME	Q8ig45 drosophila
177	167	10.8	404	2	Q4KLY3 RAT	Q4kly3 rattus norv	250	160	10.4	1051	1	PTK7 CHICK	Q91048 gallus gall

251	160	10.4	1288	2	0624K5_CABER	0624K5_caenorhabdi	324	156	10.1	387	1	STG13_PANTR	0641a4_pan troglod
252	160	10.4	1328	2	021043_CABEL	021043_caenorhabdi	325	156	10.1	865	2	068DA2_HUMAN	08af26_homo sapien
253	160	10.4	1714	2	08UVU7_XENLA	08uvu7_xenopus lae	326	156	10.1	931	2	08NFP26_HUMAN	08af26_homo sapien
254	160	10.4	2676	2	0869A0_DROME	0869a0_drosophila	327	156	10.1	997	2	044087_CABEL	044087_caenorhabdi
255	160	10.4	2898	2	0868Z9_DROME	0868z9_drosophila	328	156	10.1	1028	1	CNTN6_MOUSE	091mb8_mus muscucu
256	159.5	10.3	3987	2	06XRC3_HUMAN	06xrc3_homo sapien	329	156	10.1	1040	1	CNTN2_RAT	022063_rattus norv
257	159.5	10.3	1032	2	08UVU6_BRARE	08uvu6_brachydantio	330	156	10.1	1259	2	06PGJ3_MOUSE	06pgj3_mus muscucu
258	159.5	10.3	1056	2	090203_XENLA	090203_xenopus lae	331	156	10.1	1264	2	P91767_MANSE	P91767_manduca sex
259	159.5	10.3	1140	2	04RRD1_TETNG	04rrd1_tetradodon n	332	156	10.1	2295	2	061GU4_CABER	061gu4_caenorhabdi
260	159.5	10.3	1443	2	08MTB2_DROME	08mtb2_drosophila	333	155.5	10.1	521	2	061352_MOUSE	061352_mus muscucu
261	159.5	10.3	1765	2	09VSJ0_DROME	09vsj0_drosophila	334	155.5	10.1	525	2	05R9N6_PONPY	05r9n6_pongo pygma
262	159.5	10.3	1770	2	09VSJ2_DROME	09vsj2_drosophila	335	155.5	10.1	803	2	080ZFS_RAT	080zfs_rattus norv
263	159.5	10.3	2419	2	07PXZ1_ANOGA	07pxz1_anopheles g	336	155.5	10.1	808	1	FGFR4_MOUSE	001142_mus muscucu
264	159	10.3	326	2	04RDM1_TETNG	04rdm1_tetradodon n	337	155.5	10.1	811	2	09YH43_XENLA	09yh43_xenopus lae
265	159	10.3	326	2	09D9U0_MOUSE	09d9u0_mus muscucu	338	155.5	10.1	837	2	07Z7F2_HUMAN	07z7f2_homo sapien
266	159	10.3	340	1	NTRI_MOUSE	09p9j0_mus muscucu	339	155.5	10.1	858	1	NCAM1_RAT	P13596_rattus norv
267	159	10.3	344	2	08BG33_MOUSE	08bg33_m mus muscu	340	155.5	10.1	1499	2	090815_CHICK	090815_gallus galli
268	159	10.3	433	2	09V644_DROME	09v644_drosophila	341	155	10.0	265	2	Q9NGZ0_SPOPR	Q9ngz0_spodoptera
269	159	10.3	538	2	09OY07_MOUSE	09oy07_mus muscucu	342	155	10.0	344	2	05R554_PONPY	05r554_pongo pygma
270	159	10.3	1006	2	06IDB8_DROME	06ide8_drosophila	343	155	10.0	601	2	096CJ3_HUMAN	096cj3_homo sapien
271	159	10.3	1827	2	09VSG5_DROME	09vsg5_drosophila	344	155	10.0	641	2	086SD2_CIOIN	086sd2_clona intes
272	159	10.3	2008	2	09VEJ5_DROME	09vej5_drosophila	345	155	10.0	816	2	08NFA5_HUMAN	08nfa5_homo sapien
273	159	10.3	2046	2	07KSB3_DROME	07ksb3_drosophila	346	155	10.0	858	2	08FX47_HUMAN	08fx47_homo sapien
274	159	10.3	3347	2	08MMJ9_BOMMO	08mmj9_bombyx mori	347	155	10.0	943	2	07PRK4_HUMAN	07prk4_anopheles g
275	159	10.3	3354	2	08T101_BOMMO	08t101_bombyx mori	348	155	10.0	1070	2	0610S4_HUMAN	0610s4_homo sapien
276	158.5	10.3	330	2	P97268_CAVPO	P97268_cavia porce	349	155	10.0	1070	2	05T6S0_HUMAN	05t6s0_homo sapien
277	158.5	10.3	437	2	08NPF5_HUMAN	08nif5_homo sapien	350	155	10.0	1089	2	04S556_TETNG	04s556_tetradodon n
278	158.5	10.3	977	2	086RD9_HUMAN	086rd9_homo sapien	351	155	10.0	1280	2	04RRJ3_TETNG	04rrj3_tetradodon n
279	158.5	10.3	977	2	05VYK9_HUMAN	05vyk9_homo sapien	352	155	10.0	1748	2	04S306_TETNG	04s306_tetradodon n
280	158	10.2	875	2	04RRR9_TETNG	04rrr9_tetradodon n	353	154.5	10.0	442	2	06NM88_BRARE	06nm88_brachydantio
281	158	10.2	1040	1	CNTN2_HUMAN	002246_homo sapien	354	154.5	10.0	521	2	0925P3_MOUSE	0925p3_mus muscucu
282	158	10.2	1040	2	Q5T058_HUMAN	05t054_homo sapien	355	154.5	10.0	527	2	04SZU1_TETNG	04szu1_tetradodon n
283	158	10.2	1040	2	Q5RD18_PONPY	05rd18_pongo pygma	356	154.5	10.0	605	2	0921P2_MOUSE	0921p2_mus muscucu
284	158	10.2	1062	2	08BK63_MOUSE	08bk63_mus muscucu	357	154.5	10.0	725	2	0312D5_CANFA	0312d5_canfa
285	158	10.2	1091	1	NCAM1_CHICK	P13590_gallus galli	358	154.5	10.0	838	2	08BQ96_MOUSE	08bq96_mus muscucu
286	158	10.2	1302	1	NRG_DROME	P20241_drosophila	359	154.5	10.0	847	2	08C4B2_MOUSE	08c4b2_mus muscucu
287	158	10.2	1379	2	Q4SMF3_TETNG	Q4smf3_tetradodon n	360	154.5	10.0	838	2	0512D7_CANFA	0512d7_canis famli
288	157.5	10.2	345	2	Q58DA5_BOVIN	Q58das_bos taurus	361	154.5	10.0	1675	2	098SM4_BRARE	098sm4_brachydantio
289	157.5	10.2	433	2	Q6VAN5_BOVIN	Q6van5_bos taurus	362	154.5	10.0	1759	2	07PPH8_ANOGA	07pph8_anopheles g
290	157.5	10.2	365	2	Q6DJ83_XENTR	Q6dj83_xenopus tro	363	154.5	10.0	2053	1	DSCL1_HUMAN	08rd84_homo sapien
291	157.5	10.2	639	2	Q96P30_HUMAN	Q96p30_homo sapien	364	154.5	10.0	725	2	Q7Z2Z48_BRARE	07z2z48_brachydantio
292	157.5	10.2	707	2	Q5VXZ8_HUMAN	Q5vxz8_homo sapien	365	154	10.0	461	2	Q13854_HUMAN	013854_homo sapien
293	157.5	10.2	719	2	Q66IV0_XENLA	Q66iv0_xenopus lae	366	154	10.0	633	2	Q5M434_BRARE	05m433_brachydantio
294	157.5	10.2	725	2	Q73633_XENLA	Q73633_xenopus lae	367	154	10.0	651	2	Q5W433_BRARE	05w433_brachydantio
295	157.5	10.2	727	2	Q6RKB2_RAT	Q6rkb2_rattus norv	368	154	10.0	690	2	Q5ISL0_MACFA	05isl0_macaca fasc
296	157.5	10.2	734	2	Q96L44_HUMAN	Q96l44_homo sapien	369	154	10.0	739	1	Q5FVS3_RAT	Q5fv33_rattus norv
297	157.5	10.2	734	2	Q96P31_HUMAN	Q96p31_homo sapien	370	154	10.0	739	2	Q5FVS3_RAT	Q5fv33_rattus norv
298	157.5	10.2	742	2	Q8N6S2_HUMAN	Q8n6s2_homo sapien	371	154	10.0	761	1	NCAL12_HUMAN	P13592_homo sapien
299	157.5	10.2	837	1	NCAM2_HUMAN	013394_homo sapien	372	154	10.0	807	2	Q59FL7_HUMAN	Q59fl7_homo sapien
300	157.5	10.2	837	1	NCAM2_MOUSE	035136_mus muscucu	373	154	10.0	848	1	NCAL1_HUMAN	P13591_homo sapien
301	157.5	10.2	837	1	Q6RKB3_RAT	Q6rkb3_rattus norv	374	154	10.0	1070	1	PKY7_HUMAN	Q13308_homo sapien
302	157.5	10.2	1088	1	NCAL1_XENLA	P16170_xenopus lae	375	154	10.0	1248	2	Q9XT41_CERAE	Q9xt41_cercopithec
303	157.5	10.2	1098	2	Q4RRT1_TETNG	Q4rrt1_tetradodon n	376	154	10.0	1256	2	Q35158_RAT	Q35158_rattus norv
304	157.5	10.2	1323	2	Q08476_CHICK	Q08476_gallus galli	377	153.5	9.9	394	2	Q7ZXX1_XENLA	Q7zxx1_xenopus lae
305	157	10.2	235	2	Q4SQ01_TETNG	Q4sq01_tetradodon n	378	153.5	9.9	550	2	Q9VMN9_DROME	Q9vmn9_drosophila
306	157	10.2	337	2	P97268_CAVPO	Q97268_cavia porce	379	153.5	9.9	582	2	Q8R4B5_MOUSE	Q8r4b5_mus muscucu
307	157	10.2	344	1	NTRI_HUMAN	P91221_homo sapien	380	153.5	9.9	739	2	Q865F2_RABIT	Q865f2_cryciolagus
308	157	10.2	406	2	Q8N7T8_HUMAN	Q8n7t8_homo sapien	381	153.5	9.9	815	1	NCAM1_BOVIN	P31836_bos taurus
309	157	10.2	846	2	Q57577_CYNPY	Q57577_cynops pyrr	382	153.5	9.9	953	2	NCAM1_MOUSE	08r435_mus muscucu
310	157	10.2	1100	2	Q57576_CYNPY	Q57576_cynops pyrr	383	153.5	9.9	1043	2	Q6PA07_XENLA	Q6pa07_xenopus lae
311	157	10.2	1199	2	Q21041_CABEL	Q21041_caenorhabdi	384	153.5	9.9	1060	2	Q9QZ13_RAT	Q9qz13_rattus norv
312	157	10.2	2169	2	Q8AV58_CHICK	Q8av58_gallus galli	385	153.5	9.9	1209	2	Q7PG72_ANOGA	Q7pg72_anopheles g
313	156.5	10.1	208	2	Q80WN3_MOUSE	Q80wn3_mus muscucu	386	153.5	9.9	1215	2	Q7QBC1_ANOGA	Q7qbc1_anopheles g
314	156.5	10.1	300	2	Q68SP0_MOUSE	Q68sp0_mus muscucu	387	153.5	9.9	2024	2	Q53CM6_BRARE	Q53cm6_brachydantio
315	156.5	10.1	345	2	Q81IHT_MOUSE	Q81iht_mus muscucu	388	153	9.9	344	1	NTRI_RAT	Q7G718_rattus norv
316	156.5	10.1	778	1	KIRB3_HUMAN	Q81z99_homo sapien	389	153	9.9	545	2	Q7Q1D4_ANOGA	Q7q1d4_anopheles g
317	156.5	10.1	778	1	KIRB3_MOUSE	Q8br86_mus muscucu	390	153	9.9	588	2	Q4RFR0_TETNG	Q4rfr0_tetradodon n
318	156.5	10.1	829	2	Q4RIG0_TETNG	Q4rig0_tetradodon n	391	153	9.9	590	2	Q4SPB8_TETNG	Q4spb8_tetradodon n
319	156.5	10.1	1348	2	Q677M1_CHICK	Q677m1_gallus galli	392	153	9.9	912	2	Q4S2G4_TETNG	Q4s2g4_tetradodon n
320	156.5	10.1	1386	1	ROBO3_HUMAN	Q9sm80_homo sapien	393	153	9.9	1005	2	P79921_XENLA	P79921_xenopus lae
321	156.5	10.1	2213	2	Q7Z5N4_HUMAN	Q7z5n4_homo sapien	394	153	9.9	1028	1	CNTN6_RAT	P97528_rattus norv
322	156	10.1	300	2	Q9DA22_MOUSE	Q9da22_mus muscucu	395	153	9.9	1260	1	L1CAN_MOUSE	P11627_mus muscucu
323	156	10.1	368	2	Q5UB49_HUMAN	Q5ub49_homo sapien	396	153	9.9	1338	1	VGFR1_HUMAN	P17948_h vaecular

397	153	9.9	1338	2	O5TAR1_HUMAN	O5TAR1_homo sapien	470	149.5	9.7	1030	2	O8NFA8_HUMAN	O8NFA8_homo sapien
398	152.5	9.9	342	2	O642G9_BRARE	O642G9_brachydanio	471	149.5	9.7	1497	2	O5XJV4_MOUSE	O5XJV4_mus musculus
399	152.5	9.9	354	2	O9W4R3_DROME	O9W4R3_drosophila	472	149.5	9.7	1501	2	O7TTL7_MOUSE	O7TTL7_mus musculus
400	152.5	9.9	821	2	O9YH44_XENLA	O9YH44_xenopus lae	473	149.5	9.7	1504	2	O64699_MOUSE	O64699_mus musculus
401	152.5	9.9	857	2	O5EA96_BOVIN	O5EA96_bos taurus	474	149.5	9.7	1907	2	O4JFC7_MOUSE	O4JFC7_mus musculus
402	152.5	9.9	857	2	O5I2D6_CANFA	O5I2D6_canis familiaris	475	149.5	9.7	359	1	LACH_DROME	LACH_drosophila
403	152.5	9.9	920	2	O4RS67_TETNG	O4RS67_tetodon n	476	149.5	9.7	437	2	O7OC58_ANOGA	O7OC58_anopheles g
404	152.5	9.9	1225	2	O6GPE1_XENLA	O6GPE1_xenopus lae	477	149.5	9.7	450	2	O6UXI0_HUMAN	O6UXI0_homo sapien
405	152.5	9.9	1332	2	O9BN17_DROME	O9BN17_drosophila	478	149.5	9.7	476	2	O7ZXJ8_XENLA	O7ZXJ8_xenopus lae
406	152.5	9.9	1332	2	O9VQW7_DROME	O9VQW7_drosophila	479	149.5	9.7	526	1	CEAM1_HUMAN	CEAM1_homo sapien
407	152	9.8	338	1	LSAMP_HUMAN	O13449_homo sapien	480	149.5	9.7	739	1	VCAM1_HUMAN	VCAM1_homo sapien
408	152	9.8	534	2	O8SSE4_HUMAN	O8SSE4_homo sapien	481	149.5	9.7	739	2	O53FL7_HUMAN	O53FL7_homo sapien
409	152	9.8	534	2	O866R2_PANTR	O866R2_pan troglod	482	149.5	9.7	1031	2	O90YM2_BRARE	O90YM2_brachydanio
410	152	9.8	838	2	O4SPR9_TETNG	O4SPR9_tetodon n	483	149.5	9.7	1255	2	O7YOL7_PONPY	O7YOL7_pongo pygma
411	152	9.8	891	2	O25177_HYDAT	O25177_hydat atten	484	149.5	9.7	1937	2	O7OGT8_ANOGA	O7OGT8_anopheles g
412	152	9.8	1036	1	CNTN2_CHICK	P28685_gallus gall	485	149.5	9.7	1948	1	PTPRS_HUMAN	PTPRS_homo sapien
413	152	9.8	1114	2	O9BWL1_HUMAN	O9BWL1_homo sapien	486	149.5	9.7	4391	1	PGBM_HUMAN	PGBM_HUMAN
414	152	9.8	1115	2	O6UXJ5_HUMAN	O6UXJ5_homo sapien	487	149.5	9.7	4391	2	O5VU27_HUMAN	O5VU27_homo sapien
415	152	9.8	1255	2	O7Z3Z9_HUMAN	O7Z3Z9_homo sapien	488	148.5	9.6	591	2	O4TZM0_TETNG	O4TZM0_tetodon n
416	152	9.8	1255	2	O7YQJ8_PANTR	O7YQJ8_pan troglod	489	148.5	9.6	650	2	O63709_PMURI	O63709_rattus sp.
417	152	9.8	1257	1	LICAM_HUMAN	P22004_homo sapien	490	148.5	9.6	885	2	O8HYV1_PIG	O8HYV1_sus scrofa
418	152	9.8	1443	1	NEOL_CHICK	O30610_gallus gall	491	148.5	9.6	886	2	O8HYV2_PIG	O8HYV2_sus scrofa
419	151.5	9.8	458	2	O4SY17_TETNG	O61351_mus musculus	492	148.5	9.6	955	1	MDGA1_HUMAN	MDGA1_homo sapien
420	151.5	9.8	581	2	O61351_MOUSE	O61351_mus musculus	493	148.5	9.6	972	2	O26614_STRPU	O26614_strongyloce
421	151.5	9.8	725	1	NCA12_MOUSE	P13594_mus musculus	494	148.5	9.6	1378	1	ROBO2_HUMAN	O9HCX4_homo sapien
422	151.5	9.8	740	2	O96P25_HUMAN	O96P25_homo sapien	495	148.5	9.6	1534	2	O4RRJ4_TETNG	O4RRJ4_tetodon n
423	151.5	9.8	838	2	O90WL1_BRARE	O90WL1_brachydanio	496	148.5	9.6	2224	2	O4SLN7_TETNG	O4SLN7_tetodon n
424	151.5	9.8	846	2	O5R1Q0_FELCA	O5R1Q0_felis silve	497	148.5	9.6	231	2	O22780_CAEEL	O22780_caenorhabdi
425	151.5	9.8	847	2	O5G7G8_FELCA	O5G7G8_felis silve	498	148.5	9.6	287	2	O4SLB9_TETNG	O4SLB9_tetradon n
426	151.5	9.8	1028	1	CNTN6_HUMAN	O9UG59_homo sapien	499	148.5	9.6	302	2	O7PN14_ANOGA	O7PN14_anopheles g
427	151.5	9.8	1028	2	O61NB5_XENLA	O61NB5_xenopus lae	500	148.5	9.6	606	2	O4TAK0_TETNG	O4TAK0_tetradon n
428	151.5	9.8	1033	2	O9V643_DROME	O9V643_drosophila	501	148.5	9.6	1021	2	O930J3_HUMAN	O930J3_homo sapien
429	151.5	9.8	1115	1	NCA11_MOUSE	P13595_mus musculus	502	148.5	9.6	1100	1	CNTN5_HUMAN	O94779_homo sapien
430	151.5	9.8	3707	1	PGBM_MOUSE	O57933_mus musculus	503	148.5	9.6	1406	2	O9GPP7_DROME	O9GPP7_drosophila
431	151	9.8	442	2	O6KAT6_MOUSE	O6KAT6_mus musculus	504	148.5	9.6	1463	2	O9VQ08_DROME	O9VQ08_drosophila
432	151	9.8	749	2	O967D9_DROME	O967D9_drosophila	505	148.5	9.6	1612	1	ROBO1_MOUSE	O89026_mus musculus
433	151	9.8	902	2	O81O17_DROME	O81O17_drosophila	506	147.5	9.6	1946	2	O07153_TORCA	O07153_torpedo cal
434	151	9.8	903	2	O9VOY1_DROME	O9VOY1_drosophila	507	147.5	9.6	1065	1	LRIQ2_HUMAN	O94888_homo sapien
435	151	9.8	903	2	O967D8_DROME	O967D8_drosophila	508	147.5	9.6	1092	1	NCA12_XENLA	P15363_xenopus lae
436	151	9.8	1249	2	O90Z04_XENLA	O90Z04_xenopus lae	509	147.5	9.5	333	1	AMAL_DROME	P15364_drosophila
437	151	9.8	1508	2	O6NR34_DROME	O6NR34_drosophila	510	147.5	9.5	341	2	O7KXS2_DROME	O7KXS2_drosophila
438	151	9.8	1508	2	O9VOY2_DROME	O9VOY2_drosophila	511	147.5	9.5	353	1	CEPUL_CHICK	O90773_gallus gall
439	151	9.8	1531	2	O967D7_DROME	O967D7_drosophila	512	147.5	9.5	400	2	O4TOS4_TETNG	O4TOS4_tetradon n
440	150.5	9.7	265	1	CEAW7_HUMAN	O14002_homo sapien	513	147.5	9.5	413	2	O6ZNU1_HUMAN	O6ZNU1_homo sapien
441	150.5	9.7	349	1	CEAM8_HUMAN	P11997_homo sapien	514	147.5	9.5	473	2	O5PPW7_XENLA	O5PPW7_xenopus lae
442	150.5	9.7	395	2	O8BZP4_MOUSE	O8BZP4_mus musculus	515	147.5	9.5	509	1	SHEP1_FAT	P97710_rattus norv
443	150.5	9.7	395	2	O8BXJ7_MOUSE	O8BXJ7_mus musculus	516	147.5	9.5	677	2	O7PMJ1_ANOGA	O7PMJ1_anopheles g
444	150.5	9.7	404	1	CEAMLQ9_MOUSE	O8BL19_mus musculus	517	147.5	9.5	1210	2	O59FY0_HUMAN	O59FY0_homo sapien
445	150.5	9.7	521	2	CEAM1_MOUSE	P11809_mus musculus	518	147.5	9.5	1234	2	O00533_HUMAN	O00533_homo sapien
446	150.5	9.7	1028	2	O5R6D4_PONPY	O5R6D4_pongo pygma	519	147.5	9.5	1367	2	O7POF4_ANOGA	O7POF4_anopheles g
447	150.5	9.7	1033	2	O243Z7_DROME	O243Z7_drosophila	520	147.5	9.5	1515	2	O4SHH6_TETNG	O4SHH6_tetradon n
448	150.5	9.7	1501	2	O9QW00_PMURI	O9QW00_rattus sp.	521	147.5	9.5	1898	2	O9E017_MOUSE	O9E017_mus musculus
449	150.5	9.7	1501	2	O4JFL8_RAT	O4JFL8_rattus norv	522	147.5	9.5	1933	2	O6PAL2_MOUSE	O6PAL2_mus musculus
450	150.5	9.7	1561	2	O924D2_MOUSE	O924D2_mus musculus	523	147.5	9.5	2159	2	O6PAL2_MOUSE	O6PAL2_mus musculus
451	150.5	9.7	1788	2	O9IAJ0_XENLA	O9IAJ0_xenopus lae	524	146.5	9.5	317	2	O5TON9_ANOGA	O5TON9_anopheles g
452	150.5	9.7	1863	2	O64605_RAT	O64605_rattus norv	525	146.5	9.5	341	2	O61354_MOUSE	O61354_mus musculus
453	150.5	9.7	3165	2	O7Q767_ANOGA	O7Q767_anopheles g	526	146.5	9.5	404	2	O8BYP1_MOUSE	O8BYP1_mus musculus
454	150	9.7	508	1	O90Z71_BRARE	O90Z71_brachydanio	527	146.5	9.5	454	2	O91WS4_MOUSE	O91WS4_mus musculus
455	150	9.7	702	1	CEAMS_HUMAN	O66731_homo sapien	528	146.5	9.5	1287	2	O4KMG0_HUMAN	O4KMG0_homo sapien
456	150	9.7	702	1	CEAMAD0_HUMAN	O81440_homo sapien	529	146.5	9.5	1651	1	ROBO1_HUMAN	O62220_mus musculus
457	150	9.7	702	1	CNTN2_MOUSE	O61330_mus musculus	530	146.5	9.5	1694	1	SN_MOUSE	O62220_mus musculus
458	150	9.7	2693	2	O8ISF3_CAEEL	O8ISF3_caenorhabdi	531	146.5	9.5	17903	2	O7RLL4_DROME	O7RLL4_drosophila
459	150	9.7	2708	2	O8ISF4_CAEEL	O8ISF4_caenorhabdi	532	146.5	9.5	702	2	O53G30_HUMAN	O53G30_homo sapien
460	150	9.7	16215	2	O9NFS3_DROME	O9NFS3_drosophila	533	146.5	9.5	802	1	FEFR4_HUMAN	P22435_homo sapien
461	150	9.7	18074	2	O917U4_DROME	O917U4_drosophila	534	146.5	9.5	948	2	O8TDA0_HUMAN	O8TDA0_homo sapien
462	150	9.7	18519	2	O8ISF6_CAEEL	O8ISF6_caenorhabdi	535	146.5	9.5	982	2	O9VME2_DROME	O9VME2_drosophila
463	150	9.7	18519	2	O8ISF7_CAEEL	O8ISF7_caenorhabdi	536	146.5	9.5	1259	1	LICAM_RAT	O05653_rattus norv
464	150	9.7	18534	2	O78T27_MOUSE	O78T27_mus musculus	537	146.5	9.5	1479	2	O7KOT5_DROME	O7KOT5_drosophila
465	149.5	9.7	234	2	O8B8Q7_HUMAN	O8B8Q7_homo sapien	538	146.5	9.5	1482	2	O5M799_HUMAN	O5M799_homo sapien
466	149.5	9.7	337	1	OBCAM_CHICK	O58892_gallus gall	539	146.5	9.5	1914	2	O6VZK6_CNPV	O6VZK6_cantirypox v
467	149.5	9.7	344	2	O9DF61_CHICK	O9DF61_gallus gall	540	145.5	9.4	375	2	O4S919_TETNG	O4S919_tetradon n
468	149.5	9.7	725	2	O73634_XENLA	O73634_xenopus lae	541	145.5	9.4	443	2	O9W7A9_BRARE	O9W7A9_brachydanio
469	149.5	9.7	725	2	O73634_XENLA	O73634_xenopus lae	542	145.5	9.4	443	2	O9W7A9_BRARE	O9W7A9_brachydanio

543	145.5	9.4	534	2	Q25403_LYMST	Q25403	lymaea	ata	616	143	9.3	1513	2	Q90270_BRARE	Q90270	brachydantio
544	145.5	9.4	1054	1	LRIG2_MOUSE	Q54kr2	mus	musculu	617	143	9.3	1560	1	Q59FX6_HUMAN	Q59FX6	homo sapien
545	145.5	9.4	1070	2	Q4S2F2_TETNG	Q4S2F2	tetradon	n	618	143	9.3	1914	1	MTLK_HUMAN	Q51746	homo sapien
546	145.5	9.4	1470	1	ROBO2_MOUSE	Q7Pdp3	mus	musculu	619	143	9.3	1946	2	Q68J72_APIME	Q68J72	apis mellif
547	145	9.4	313	2	Q57596_CHICK	Q57596	gallus	gall1	620	143	9.3	2331	2	Q59EG0_HUMAN	Q59EG0	homo sapien
548	145	9.4	315	2	Q9DGI5_CHICK	Q9DGI5	gallus	gall1	621	143	9.3	2604	1	Q4ZG20_HUMAN	Q4ZG20	homo sapien
549	145	9.4	344	2	Q93242_CHICK	Q93242	gallus	gall1	622	143	9.3	5604	2	Q8W253_HUMAN	Q8W253	homo sapien
550	145	9.4	601	2	Q4VWU5_CHICK	Q4VWU5	xenopus	lae	623	143	9.3	26926	2	Q4U126_HUMAN	Q4U126	homo sapien
551	145	9.4	1108	2	Q5RUH4_MOUSE	Q5RUH4	mus	musculu	624	143	9.3	26926	2	Q8W253_HUMAN	Q8W253	homo sapien
552	145	9.4	1377	1	NEO1_RAT	P97603	rattus	norv	625	142.5	9.2	278	1	Q99232_MOUSE	Q99232	mus musculu
553	145	9.4	1912	1	PTPRD_HUMAN	P23460	homo sapien		626	142.5	9.2	388	1	BASI_CHICK	Q92372	chicken
554	145	9.4	1914	2	Q7Z4U0_HUMAN	Q7Z4U0	homo sapien		627	142.5	9.2	524	2	Q7PS78_ANOGA	Q7PS78	anopheles g
555	144.5	9.4	242	2	Q5TNJ9_ANOGA	Q5tnu9	anopheles	g	628	142.5	9.2	640	2	Q8BSM2_MOUSE	Q8BSM2	mouse
556	144.5	9.4	349	1	LACH_SCNAM	Q24474	schistocerc		629	142.5	9.2	815	2	Q8AYP3_BRARE	Q8AYP3	brachydantio
557	144.5	9.4	536	2	Q4VSE0_DROME	Q4VSE0	drosophila		630	142.5	9.2	1034	2	Q5TF58_HUMAN	Q5TF58	homo sapien
558	144.5	9.4	606	2	Q4VNM6_DROME	Q4VNM6	drosophila		631	142.5	9.2	1034	2	Q59F30_HUMAN	Q59F30	homo sapien
559	144.5	9.4	626	2	Q53HD1_HUMAN	Q53hd1	homo sapien		632	142.5	9.2	1261	2	Q4JPL6_RAT	Q4JPL6	rattus norv
560	144.5	9.4	646	2	Q8NH8_HUMAN	Q8nh8	homo sapien		633	142.5	9.2	1379	2	Q5XNV9_PETMA	Q5XNV9	petromyzon
561	144.5	9.4	1336	1	VGPR1_RAT	P53767	rattus	norv	634	142.5	9.2	1415	2	Q5XNV8_PETMA	Q5XNV8	petromyzon
562	144.5	9.4	1484	1	Q5W9G3_HUMAN	Q5W9G3	homo sapien		635	142.5	9.2	1495	2	Q4URJ3_RAT	Q4URJ3	rattus norv
563	144.5	9.4	1897	1	PTPRF_HUMAN	P10586	homo sapien		636	142.5	9.2	1949	2	Q6PDU3_MOUSE	Q6PDU3	mouse
564	144.5	9.4	1898	2	Q8W6S0_HUMAN	Q8W6S0	homo sapien		637	142.5	9.2	4129	2	Q59E65_DROME	Q59E65	drosophila
565	144.5	9.4	1898	2	Q5T021_HUMAN	Q5T021	homo sapien		638	142	9.2	294	2	Q8BH36_MESAU	Q8BH36	mesocricetu
566	144.5	9.4	1903	2	Q5SRJ6_MOUSE	Q5SRJ6	mus musculu		639	142	9.2	373	2	Q7KYP5_HUMAN	Q7KYP5	homo sapien
567	144.5	9.4	1907	2	Q5T022_HUMAN	Q5T022	homo sapien		640	142	9.2	388	2	Q9Z151_MOUSE	Q9Z151	mus musculu
568	144.5	9.4	1918	2	Q5W9G2_HUMAN	Q5W9G2	homo sapien		641	142	9.2	434	2	Q6DN72_HUMAN	Q6DN72	homo sapien
569	144	9.3	301	2	Q7Q864_ANOGA	Q7Q864	anopheles	g	642	142	9.2	464	2	Q61710_HUMAN	Q61710	homo sapien
570	144	9.3	316	2	Q8WP58_DROSI	Q8WP58	drosophila		643	142	9.2	468	2	Q96CA7_HUMAN	Q96CA7	homo sapien
571	144	9.3	316	2	Q8WP94_DROSI	Q8WP94	drosophila		644	142	9.2	509	2	Q9E0Y5_MOUSE	Q9E0Y5	m mman-g pr
572	144	9.3	316	2	Q8WP93_DROSI	Q8WP93	drosophila		645	142	9.2	617	2	Q5IF12_BRARE	Q5IF12	brachydantio
573	144	9.3	318	2	Q6PC47_HUMAN	Q6PC47	homo sapien		646	142	9.2	913	2	Q8T3E5_CAEEL	Q8T3E5	caenorhabdi
574	144	9.3	353	2	Q8KX13_HUMAN	Q8KX13	homo sapien		647	142	9.2	928	2	Q91218_CAEEL	Q91218	caenorhabdi
575	144	9.3	519	1	CEAM1_RAT	P16573	rattus	norv	648	142	9.2	955	2	Q8MQ66_CAEEL	Q8MQ66	caenorhabdi
576	144	9.3	582	2	Q80WN2_MOUSE	Q80wn2	mus musculu		649	142	9.2	978	2	Q5TYT0_BRARE	Q5TYT0	brachydantio
577	144	9.3	595	2	Q6S8N8_MOUSE	Q6S8N8	mus musculu		650	142	9.2	1027	1	CNTN5_CHICK	CNTN5	chicken
578	144	9.3	719	2	Q9U4G1_DROME	Q9U4G1	mus musculu		651	142	9.2	1031	2	Q597F7_BRARE	Q597F7	brachydantio
579	144	9.3	868	1	MUSK_MOUSE	Q61006	mus musculu		652	142	9.2	1239	2	Q61PR2_CAEEL	Q61PR2	caenorhabdi
580	144	9.3	1098	1	CNTN5_MOUSE	P68500	mus musculu		653	142	9.2	1285	2	Q5TYT1_BRARE	Q5TYT1	brachydantio
581	144	9.3	1249	2	Q4RTM9_RAT	Q4RTM9	rattus	norv	654	142	9.2	1905	2	Q5VY19_HUMAN	Q5VY19	homo sapien
582	144	9.3	1301	2	Q4RSG5_TETNG	Q4RSG5	tetradon	n	655	142	9.2	2752	2	Q7QKD0_ANOGA	Q7QKD0	anopheles g
583	144	9.3	1340	2	Q5U176_DROME	Q5U176	drosophila		656	141.5	9.2	337	2	Q5D095_MOUSE	Q5D095	mus musculu
584	144	9.3	1366	1	ROBO3_MOUSE	Q9Z214	mus musculu		657	141.5	9.2	338	1	LSAMP_CHICK	LSAMP	chicken
585	144	9.3	1624	2	Q53ZG4_XENLA	Q53ZG4	xenopus	lae	658	141.5	9.2	341	1	LSAMP_MOUSE	LSAMP	mouse
586	144	9.3	1898	2	Q64604_RAT	Q64604	rattus	norv	659	141.5	9.2	349	2	Q7QUG1_ANOGA	Q7QUG1	anopheles g
587	144	9.3	2403	2	Q8MLD5_DROME	Q8MLD5	drosophila		660	141.5	9.2	361	2	Q5M960_RAT	Q5M960	rattus norv
588	144	9.3	4463	2	Q8MLD8_DROME	Q8MLD8	drosophila		661	141.5	9.2	468	2	Q6PJ50_MOUSE	Q6PJ50	mus musculu
589	144	9.3	7210	2	Q9V7G8_DROME	Q9V7G8	drosophila		662	141.5	9.2	567	1	ILRL1_MOUSE	ILRL1	mouse
590	144	9.3	9270	2	Q8MLD9_DROME	Q8MLD9	drosophila		663	141.5	9.2	582	2	Q56784_HUMAN	Q56784	homo sapien
591	143.5	9.3	208	2	Q866T1_PONPY	Q866T1	pongo	pygma	664	141.5	9.2	626	1	MAG_HUMAN	MAG	homo sapien
592	143.5	9.3	337	2	Q6GLZ7_XENLA	Q6GLZ7	xenopus	lae	665	141.5	9.2	626	2	Q53BS7_HUMAN	Q53BS7	homo sapien
593	143.5	9.3	435	2	Q8N3J6_HUMAN	Q8N3J6	homo sapien		666	141.5	9.2	661	2	Q5R4C0_PONPY	Q5R4C0	pongo pygma
594	143.5	9.3	437	2	Q81ZP8_HUMAN	Q81ZP8	homo sapien		667	141.5	9.2	667	2	Q59GD9_HUMAN	Q59GD9	homo sapien
595	143.5	9.3	467	1	SIGL1_MOUSE	Q9VY57	mus musculu		668	141.5	9.2	1026	1	CNTN4_RAT	CNTN4	rattus norv
596	143.5	9.3	504	1	RCRL1_MOUSE	Q8H441	homo sapien		669	141.5	9.2	1066	2	Q8MSR5_DROME	Q8MSR5	drosophila
597	143.5	9.3	617	2	Q5MY54_BRARE	Q5MY54	brachydantio		670	141.5	9.2	1465	2	Q7TQO5_MOUSE	Q7TQO5	mouse
598	143.5	9.3	817	2	Q8JY38_BRARE	Q8JY38	brachydantio		671	141.5	9.2	1493	1	NEO1_MOUSE	NEO1	mouse
599	143.5	9.3	1845	2	Q5MYA0_HUMAN	Q5MYA0	homo sapien		672	141.5	9.2	1651	1	PTPRD_MOUSE	PTPRD	mouse
600	143.5	9.3	1887	2	Q9Q6M7_9MURI	Q9Q6M7	rattus	bp.	673	141.5	9.2	1894	1	Q80VY8_MOUSE	Q80VY8	mouse
601	143	9.3	206	2	Q03679_MOUSE	Q03679	mus musculu		674	141.5	9.2	1950	2	Q8IRV7_DROME	Q8IRV7	drosophila
602	143	9.3	245	2	Q56UH5_PETMA	Q56UH5	petromyzon		675	141.5	9.2	3215	2	Q8IRV9_DROME	Q8IRV9	drosophila
603	143	9.3	287	2	Q13984_HUMAN	Q13984	homo sapien		676	141.5	9.2	4117	2	Q8IRV9_DROME	Q8IRV9	drosophila
604	143	9.3	325	2	Q8HW98_MOUSE	Q8HW98	mus musculu		677	141.5	9.2	4179	2	Q9W4Y4_DROME	Q9W4Y4	drosophila
605	143	9.3	338	1	LSAMP_RAT	Q62813	rattus	norv	678	141.5	9.2	4223	2	Q8MPJ3_DROME	Q8MPJ3	drosophila
606	143	9.3	347	2	Q6PJ52_HUMAN	Q6PJ52	homo sapien		679	141.5	9.2	4228	2	Q8IRV8_DROME	Q8IRV8	drosophila
607	143	9.3	377	2	Q5TNJ9_ANOGA	Q5tnu9	anopheles	g	680	141	9.1	292	2	Q5HZR6_XENLA	Q5HZR6	xenopus lae
608	143	9.3	450	2	Q5TVR25_DROME	Q5TVR25	drosophila		681	141	9.1	312	2	Q4SUX1_TETNG	Q4SUX1	tetradon n
609	143	9.3	513	1	SHPS1_MOUSE	P97797	m tyrosine-		682	141	9.1	350	2	Q02869_CHICK	Q02869	gallus gall
610	143	9.3	603	2	Q4SEN2_TETNG	Q4SEN2	tetradon	n	683	141	9.1	440	2	Q6ZMD4_HUMAN	Q6ZMD4	homo sapien
611	143	9.3	766	2	Q4RH71_TETNG	Q4RH71	tetradon	n	684	141	9.1	647	2	Q50317_BRARE	Q50317	brachydantio
612	143	9.3	907	2	Q9NEG0_DROME	Q9NEG0	drosophila		685	141	9.1	739	2	Q5R847_PONPY	Q5R847	pongo pygma
613	143	9.3	1010	1	CNTN1_CHICK	P14781	gallus	gall1	686	141	9.1	773	2	Q59FV9_HUMAN	Q59FV9	homo sapien
614	143	9.3	1277	1	L1CAM_FUGRU	Q98902	figu	rubrip	687	141	9.1	868	1	MUSK_RAT	MUSK	rattus norv
615	143	9.3	1502	2	Q9UM81_HUMAN	Q9um81	homo sapien		688	141	9.1	901	2	Q4SBD4_TETNG	Q4SBD4	tetradon n

689	141	9.1	1319	2	Q4TB2_TETNG	Q48b2 tetraodon n	762	138.5	9.0	875	2	Q4RK6_TETNG	Q4rk6 tetraodon n
690	141	9.1	1461	1	NEOI_HUMAN	Q9859 homo sapien	763	138.5	9.0	878	2	Q9GV22_MYTG	Q9gv22 mytilus gal
691	141	9.1	2174	2	Q7OEG7_ANOGA	Q7eg7 anopheles g	764	138.5	9.0	900	2	Q4SR23_TETNG	Q4sr23 tetraodon n
692	140.5	9.1	390	2	Q6KX2_XENLA	Q6kx2 xenopus lae	765	138.5	9.0	940	2	Q8NPA7_HUMAN	Q8npa7 homo sapien
693	140.5	9.1	394	2	Q8HXR9_MACMU	Q8hxr9 macaca mul	766	138.5	9.0	988	2	Q95R27_DROME	Q95r27 drosophila
694	140.5	9.1	394	2	Q8HXR7_MACPA	Q8hxr7 macaca fasc	767	138.5	9.0	998	2	Q9M4Y6_DROME	Q9m4y6 drosophila
695	140.5	9.1	428	2	Q96P6_HUMAN	Q96p6 homo sapien	768	138.5	9.0	1133	2	Q4T6P9_TETNG	Q4t6p9 tetraodon n
696	140.5	9.1	429	2	Q96LA6_HUMAN	Q96la6 homo sapien	769	138.5	9.0	1342	2	Q9GPP6_DROME	Q9gpp6 drosophila
697	140.5	9.1	465	2	Q59E14_DROME	Q59e14 drosophila	770	138.5	9.0	1342	2	Q9VPS2_DROME	Q9vps2 drosophila
698	140.5	9.1	476	2	Q4VB00_FAT	Q4vb00 rattus norv	771	138.5	9.0	1879	2	Q7OAX2_ANOGA	Q7oax2 anopheles g
699	140.5	9.1	551	2	Q8NHN7_HUMAN	Q8nhn7 homo sapien	772	138.5	9.0	1995	2	Q5TMM7_ANOGA	Q5tmm7 anopheles g
700	140.5	9.1	762	2	Q71TW8_HUMAN	Q71tw8 homo sapien	773	138.5	9.0	2000	2	Q97791_RABIT	Q97791 mytilus gal
701	140.5	9.1	773	2	Q6IDB4_DROME	Q6ide4 drosophila	774	138.5	9.0	4736	2	Q7YT99_MYTG	Q7yt99 mytilus gal
702	140.5	9.1	807	2	Q6NY23_BRARE	Q6ny23 brachydanio	775	138	8.9	204	2	Q7P4Y5_ANOGA	Q7p4y5 anopheles g
703	140.5	9.1	873	1	PAS2_DROME	P3082 drosophila	776	138	8.9	330	2	Q61341_RAT	Q61341 rattus norv
704	140.5	9.1	1026	1	CNTN4_HUMAN	Q81wv2 homo sapien	777	138	8.9	360	2	Q8NRE6_DROME	Q8nre6 drosophila
705	140.5	9.1	1264	2	Q14631_HUMAN	Q14631 homo sapien	778	138	8.9	366	2	Q8N759_HUMAN	Q8n759 homo sapien
706	140.5	9.1	1348	1	VGFR2_COTJA	P52583 coturnix co	779	138	8.9	438	2	Q4RKFS_TETNG	Q4rkfs tetraodon n
707	140.5	9.1	1478	2	Q59H90_HUMAN	Q59h90 homo sapien	780	138	8.9	478	2	Q4RVM0_TETNG	Q4rvm0 tetraodon n
708	140	9.1	218	2	Q7RJ18_ANOGA	Q7rj18 anopheles g	781	138	8.9	507	2	Q5KAQ3_PIG	Q5kaq3 sus scrofa
709	140	9.1	299	2	Q7Q0P9_ANOGA	Q7q0p9 anopheles g	782	138	8.9	510	2	Q5E929_BOVIN	Q5e929 bos taurus
710	140	9.1	509	2	Q91YK7_MOUSE	Q91yk7 mus musculu	783	138	8.9	517	2	FVR1_HUMAN	FVR1_HUMAN
711	140	9.1	626	2	Q5E9N1_BOVIN	Q5e9n1 bos taurus	784	138	8.9	723	2	Q5H2F8_XENLA	Q5h2f8 xenopus lae
712	140	9.1	628	2	Q9MZ08_BOVIN	Q9mz08 bos taurus	785	138	8.9	727	2	Q5W5X8_XENLA	Q5w5x8 xenopus lae
713	140	9.1	648	2	Q9EP1_MOUSE	Q9epf1 mus musculu	786	138	8.9	766	2	Q4SR20_TETNG	Q4sr20 tetraodon n
714	140	9.1	735	2	Q8MWS2_DROME	Q8mws2 drosophila	787	138	8.9	880	1	TYRQ3_MOUSE	TYRQ3_MOUSE
715	140	9.1	774	2	Q9V930_DROME	Q9v930 drosophila	788	138	8.9	952	2	Q6NZM6_MOUSE	Q6nzm6 mus musculu
716	140	9.1	821	2	Q4S2G2_TETNG	Q4s2g2 tetraodon n	789	138	8.9	952	2	Q4SPY1_TETNG	Q4spy1 tetraodon n
717	140	9.1	890	1	Q86VR3_HUMAN	Q86v3 homo sapien	790	138	8.9	1021	1	CNTN1_FAT	CNTN1_FAT
718	140	9.1	890	2	Q59FM9_HUMAN	Q59fm9 homo sapien	791	138	8.9	1028	1	CNTN3_HUMAN	CNTN3_HUMAN
719	140	9.1	951	2	Q5G1R7_BRARE	Q5g1r7 brachydanio	792	137.5	8.9	158	2	Q15229_HUMAN	Q15229 homo sapien
720	140	9.1	1272	2	Q4RJ21_TETNG	Q4rj21 tetraodon n	793	137.5	8.9	358	2	Q90490_BRARE	Q90490 brachydanio
721	140	9.1	1702	2	Q4S805_TETNG	Q4s805 tetraodon n	794	137.5	8.9	394	2	Q6UXG0_HUMAN	Q6uxg0 homo sapien
722	140	9.1	2095	2	Q8NBY8_HUMAN	Q8nbu8 homo sapien	795	137.5	8.9	405	2	Q6PFR4_BRARE	Q6pfr4 brachydanio
723	139.5	9.0	324	2	Q8NC17_HUMAN	Q8nc17 homo sapien	796	137.5	8.9	515	1	FVR1_PIG	FVR1_PIG
724	139.5	9.0	426	1	PSGC_HUMAN	Q9h85 drosophila	797	137.5	8.9	979	2	Q596X0_CARAU	Q596x0 carassius a
725	139.5	9.0	426	1	PSGC_HUMAN	Q9h85 drosophila	798	137.5	8.9	1029	2	Q4RVM2_TETNG	Q4rvm2 tetraodon n
726	139.5	9.0	939	1	ROBO4_FAT	Q8w87 rattus norv	799	137.5	8.9	1237	2	Q61OC8_CAEBR	Q61oc8 caenorhabd
727	139.5	9.0	961	1	Q9VQM1_DROME	Q9vqm1 drosophila	800	137.5	8.9	1237	2	Q8NHN3_HUMAN	Q8nhn3 homo sapien
728	139.5	9.0	1193	2	Q96KFS_HUMAN	Q96kf5 homo sapien	801	137.5	8.9	2212	2	Q6BBQ6_CAEBL	Q6bbq6 caenorhabd
729	139.5	9.0	1320	2	Q5V3P5_HUMAN	Q5v3p5 homo sapien	802	137.5	8.9	2389	2	Q5UJ38_BRARE	Q5uj38 brachydanio
730	139.5	9.0	1320	2	Q8N314_HUMAN	Q8n314 homo sapien	803	137	8.9	389	2	Q5K373_BRARE	Q5k373 brachydanio
731	139.5	9.0	1391	2	Q7QJX9_ANOGA	Q7qjx9 anopheles g	804	137	8.9	481	2	Q5K374_BRARE	Q5k374 brachydanio
732	139.5	9.0	3317	2	Q7PWX9_ANOGA	Q7pwx9 anopheles g	805	137	8.9	481	2	Q6BE00_XENLA	Q6be00 xenopus lae
733	139.5	9.0	7105	2	Q95YM2_PROCL	Q95ym2 procambatus	806	137	8.9	484	2	Q4RM24_TETNG	Q4rm24 tetraodon n
734	139.5	9.0	17352	2	Q6UY47_HUMAN	Q6uy47 homo sapien	807	137	8.9	489	2	MAG_MOUSE	MAG_MOUSE
735	139	9.0	296	2	Q8MM22_PIG	Q8mm22 sus scrofa	808	137	8.9	626	1	MAG_MOUSE	MAG_MOUSE
736	139	9.0	316	2	Q5YCY7_BRARE	Q5ycy7 brachydanio	809	137	8.9	648	2	Q9EPF2_RAT	Q9epf2 rattus norv
737	139	9.0	316	2	Q5YCY7_BRARE	Q5ycy7 brachydanio	810	137	8.9	648	2	Q9EPF2_RAT	Q9epf2 rattus norv
738	139	9.0	416	2	Q7Q1Z7_ANOGA	Q7q1z7 anopheles g	811	137	8.9	1026	1	CNTN4_MOUSE	CNTN4_MOUSE
739	139	9.0	416	2	Q8R212_MOUSE	Q8r2y2 mus musculu	812	137	8.9	1180	2	Q5IS40_PANTR	Q5is40 pan troglod
740	139	9.0	648	2	Q8R212_MOUSE	Q8r2y2 mus musculu	813	137	8.9	1189	2	Q9P2J2_HUMAN	Q9p2j2 homo sapien
741	139	9.0	723	2	Q8VZW7_HUMAN	Q8vzw7 homo sapien	814	137	8.9	1304	1	NRGAM_HUMAN	Q92823 homo sapien
742	139	9.0	867	2	Q5VZW7_HUMAN	Q5vzw7 homo sapien	815	137	8.9	1304	1	VGFR1_MOUSE	P35969 mus musculu
743	139	9.0	869	1	MUSK_HUMAN	Q5146 homo sapien	816	137	8.9	1535	2	Q23391_DROME	Q23391 drosophila
744	139	9.0	875	2	Q5VZM8_HUMAN	Q5vzm8 homo sapien	817	137	8.9	1944	2	Q4SPG3_TETNG	Q4spg3 tetraodon n
745	139	9.0	922	2	Q90413_BRARE	Q90413 brachydanio	818	137	8.9	4071	2	Q7PH68_ANOGA	Q7ph68 anopheles g
746	139	9.0	1020	1	CNTN1_MOUSE	P12960 mus musculu	819	137	8.9	4098	2	Q7PQ99_ANOGA	Q7pq99 anopheles g
747	139	9.0	1270	2	Q9U3P2_CAEBL	Q9u3p2 caenorhabd	820	136.5	8.8	330	2	Q90242_CHICK	Q90242 gallus gall
748	139	9.0	1272	2	Q4JDD5_BRARE	Q4jdd5 brachydanio	821	136.5	8.8	341	1	OPCM_BOVIN	Q61353 mouse
749	139	9.0	1723	2	Q8CHB2_MOUSE	Q8chb2 mus musculu	822	136.5	8.8	345	1	Q61353_MOUSE	Q61353 mouse
750	139	9.0	1843	2	Q4SPF7_TETNG	Q4spf7 tetraodon n	823	136.5	8.8	377	2	Q9VOY0_DROME	Q9voy0 drosophila
751	139	9.0	1896	2	Q91AJ1_XENLA	Q91aj1 xenopus lae	824	136.5	8.8	393	2	Q8HXR8_DERAE	Q8hxr8 ceropophilac
752	139	9.0	4648	2	Q4T3W5_TETNG	Q4t3w5 tetraodon n	825	136.5	8.8	532	2	Q6NNU3_DROME	Q6nnu3 drosophila
753	138.5	9.0	288	2	Q9TB99_PIG	Q9tbt0 sus scrofa	826	136.5	8.8	532	2	Q9VLF0_DROME	Q9vlf0 drosophila
754	138.5	9.0	297	2	Q8BE99_PIG	Q8be99 sus scrofa	827	136.5	8.8	557	2	Q4RBS2_TETNG	Q4rbs2 tetraodon n
755	138.5	9.0	335	1	PSG5_HUMAN	Q15238 homo sapien	828	136.5	8.8	570	2	Q8NCE6_HUMAN	Q8nce6 homo sapien
756	138.5	9.0	345	2	Q6GMB8_XENLA	Q6gmb8 xenopus lae	829	136.5	8.8	686	2	Q7PQW9_ANOGA	Q7pqw9 anopheles g
757	138.5	9.0	419	2	Q96QUS_HUMAN	Q96qis homo sapien	830	136.5	8.8	713	2	Q90330_COTCO	Q90330 coturnix co
758	138.5	9.0	467	2	Q4R5D0_MACPA	Q4r5p0 macaca fasc	831	136.5	8.8	771	2	Q4KM07_HUMAN	Q4km07 homo sapien
759	138.5	9.0	626	2	Q6DCH3_XENLA	Q6dch3 xenopus lae	832	136.5	8.8	851	2	Q7Q0S6_ANOGA	Q7q0s6 anopheles g
760	138.5	9.0	815	2	Q80S89_BRARE	Q80s89 brachydanio	833	136.5	8.8	956	1	MANC1_HUMAN	Q7z553 homo sapien
761	138.5	9.0	862	2	Q4SAP3_TETNG	Q4sap3 tetraodon n	834	136.5	8.8	1056	1	CNTN5_BRARE	Q7zaw4 brachydanio

835	136.5	8.8	1150	2	Q4SLB2_TETNG	Q4E182_tetractodon n	908	133.5	8.6	333	1	CD226_MOUSE	Q8K4F0_mus musculus
836	136.5	8.8	1271	2	Q6U714_BARRE	Q6U714_brachydantio	909	133.5	8.6	333	2	Q5DM6G_MOUSE	Q6M6W9_mus musculus
837	136.5	8.8	1280	2	Q90933_CHICK	Q90933_gallus galli	910	133.5	8.6	410	2	Q6R3M0_BOWMO	Q6C3M0_bombyx mori
838	136.5	8.8	3375	1	UNC52_CAEEL	Q06561_cenorhabdi	911	133.5	8.6	410	2	Q7YZA7_BOWMO	Q7YZA7_bombyx mori
839	136	8.8	229	2	Q9TT71_PIG	Q9CT13_sus scrofa	912	133.5	8.6	419	1	PSG1_HUMAN	P11464_homo sapien
840	136	8.8	230	2	Q9N213_PIG	Q9N213_sus scrofa	913	133.5	8.6	426	1	Q6ICR4_HUMAN	Q6ICR4_homo sapien
841	136	8.8	510	2	Q96K15_HUMAN	Q96K15_homo sapien	914	133.5	8.6	428	2	Q9BRW2_HUMAN	Q9BRW2_homo sapien
842	136	8.8	510	2	Q96KN8_HUMAN	Q96KN8_homo sapien	915	133.5	8.6	501	2	Q6O147_BOVIN	Q6O147_bos taurus
843	136	8.8	515	1	PVRI_MOUSE	Q9J1K6_mus musculus	916	133.5	8.6	618	2	Q4SHD7_TETNG	Q4SHD7_tetractodon n
844	136	8.8	515	1	Q6P9M9_MOUSE	Q6P9M9_mus musculus	917	133.5	8.6	626	2	Q53HAI_HUMAN	Q53HAI_homo sapien
845	136	8.8	661	2	Q5RJW1_MOUSE	Q5CJW1_mus musculus	918	133.5	8.6	632	2	Q6ZRK5_HUMAN	Q6ZRK5_homo sapien
846	136	8.8	754	2	Q8B276_MOUSE	Q8B276_m mus muscu	919	133.5	8.6	729	2	Q63A82_RAT	Q63A82_rattus norv
847	136	8.8	813	1	PUNC_MOUSE	Q8BPQ3_mus musculus	920	133.5	8.6	763	2	Q95YWG_HALRO	Q95YWG_haloecythia
848	136	8.8	814	1	PUNC_HUMAN	Q8IYU1_homo sapien	921	133.5	8.6	949	1	MAMC1_RAT	P60756_rattus norv
849	136	8.8	1045	2	Q86T37_HUMAN	Q86T37_homo sapien	922	133.5	8.6	949	1	Q4SLB3_TETNG	Q4SLB3_tetractodon n
850	136	8.8	1045	2	Q5VV36_HUMAN	Q5VV36_homo sapien	923	133.5	8.6	1250	2	Q8TDY8_HUMAN	Q8TDY8_homo sapien
851	136	8.8	1320	2	Q86TC9_HUMAN	Q86TC9_homo sapien	924	133.5	8.6	1250	2	Q88971_HUMAN	Q88971_mus musculus
852	136	8.8	1376	2	Q5DTJ9_MOUSE	Q5dctj9_mus musculus	925	133	8.6	223	2	Q7QC47_ANOGA	Q7qch7_anopheles g
853	135.5	8.8	265	2	Q02280_CAEEL	Q02280_cenorhabdi	926	133	8.6	239	2	Q4SPD7_TETNG	P79757_gallus galli
854	135.5	8.8	306	2	Q9R129_MOUSE	Q9I129_mus musculus	927	133	8.6	337	2	Q6DFY2_MOUSE	Q6dfy2_mus musculus
855	135.5	8.8	410	2	Q6R3M2_BOWMO	Q6C3M2_bombyx mori	928	133	8.6	354	2	Q5R645_PONPY	Q5r645_pongo pygma
856	135.5	8.8	442	1	S1GLE_HUMAN	Q43699_homo sapien	929	133	8.6	428	1	PSG3_HUMAN	Q6UXJ4_homo sapien
857	135.5	8.8	466	2	Q95S10_DROME	Q95S10_drosophila	930	133	8.6	477	2	Q6UXJ4_HUMAN	Q6UXJ4_homo sapien
858	135.5	8.8	782	2	Q4S143_TETNG	Q4S143_tetractodon n	931	133	8.6	1021	2	P79757_CHICK	P79757_gallus galli
859	135.5	8.8	820	2	Q5R803_PONPY	Q5R803_pongo pygma	932	133	8.6	1311	2	Q6G1K8_DROME	Q6G1K8_drosophila
860	135.5	8.8	1212	2	Q95TGO_DROME	Q95TGO_drosophila	933	133	8.6	1527	2	Q9VZ24_DROME	Q9VZ24_drosophila
861	135.5	8.8	1345	2	Q4VCDO_MOUSE	Q4VCDO_mus musculus	934	133	8.6	5724	2	Q7PT04_ANOGA	Q7PT04_anopheles g
862	135.5	8.8	1367	1	VGFR2_MOUSE	P35918_mus musculus	935	132.5	8.6	182	2	Q15108_HUMAN	Q15108_homo sapien
863	135.5	8.8	1598	2	Q9P214_HUMAN	Q9P214_homo sapien	936	132.5	8.6	189	2	Q15106_HUMAN	Q15106_homo sapien
864	135.5	8.8	531	2	Q659F2_HUMAN	Q659F2_homo sapien	937	132.5	8.6	278	2	Q61350_MOUSE	Q61350_mus musculus
865	135	8.7	659	2	Q6ZNM1_HUMAN	Q6ZNM1_homo sapien	938	132.5	8.6	302	2	Q5FM89_MOUSE	Q5FM89_mus musculus
866	135	8.7	660	2	Q7Z6M1_HUMAN	Q7Z6M1_homo sapien	939	132.5	8.6	319	2	Q5ISM6_MACRA	Q5ISM6_macaca fasc
867	135	8.7	676	2	Q4SIF9_TETNG	Q4SIF9_tetractodon n	940	132.5	8.6	410	2	Q6R3I9_BOWMA	Q6R3I9_bombyx mand
868	135	8.7	880	1	TYR03_RAT	Q4E1F9_tetractodon n	941	132.5	8.6	483	2	Q9DBP8_MOUSE	Q9dbp8_mus musculus
869	135	8.7	1154	2	Q9QVN3_9MURI	Q9QVN3_rattus norv	942	132.5	8.6	508	2	Q8CED8_MOUSE	Q8CED8_mus musculus
870	135	8.7	1235	2	Q95428_HUMAN	Q95428_homo sapien	943	132.5	8.6	508	2	Q8R007_MOUSE	Q8R007_mus musculus
871	135	8.7	1256	1	NRCAM_MOUSE	Q8I0U4_mus musculus	944	132.5	8.6	822	1	GFGR1_RAT	GFGR1_rattus norv
872	135	8.7	1278	2	Q4SM90_TETNG	Q4SM90_tetractodon n	945	132.5	8.6	1012	1	ROBO4_MOUSE	Q8C310_mus musculus
873	135	8.7	3084	2	Q4RE88_TETNG	Q4RE88_tetractodon n	946	132.5	8.6	1173	2	Q6NR54_DROME	Q6NR54_drosophila
874	134.5	8.7	180	2	Q15107_HUMAN	Q15107_homo sapien	947	132.5	8.6	1278	2	Q4R8S5_TETNG	Q4R8S5_tetractodon n
875	134.5	8.7	322	2	Q4SHQ7_TETNG	Q4shq7_tetractodon n	948	132	8.5	308	2	Q68EVL_XENLA	Q68EVL_xenopus lae
876	134.5	8.7	370	2	Q6MZ03_HUMAN	Q6mz03_homo sapien	949	132	8.5	345	2	Q5ISA8_9PRIM	Q5ISA8_saimiri bol
877	134.5	8.7	398	1	SIRB1_HUMAN	Q00241_homo sapien	950	132	8.5	345	1	OPCM_HUMAN	Q14982_homo sapien
878	134.5	8.7	410	2	Q4FART1_BOWMO	Q4FART1_bombyx mori	951	132	8.5	345	1	OPCM_PANTR	Q51861_pan troglod
879	134.5	8.7	411	2	Q15228_HUMAN	Q15228_homo sapien	952	132	8.5	345	1	OPCM_RAT	P32736_rattus norv
880	134.5	8.7	419	2	Q68CR6_MOUSE	Q68CR6_homo sapien	953	132	8.5	405	2	Q7PRJ5_ANOGA	Q7PRJ5_anopheles g
881	134.5	8.7	688	2	Q8K1H4_MOUSE	Q8K1H4_mus musculus	954	132	8.5	474	2	Q5FV48_FUGRU	Q5FV48_fugu rubrip
882	134.5	8.7	688	2	Q55095_MOUSE	Q55095_mus musculus	955	132	8.5	484	2	Q5OSL1_XENTR	Q5OSL1_xenopus tro
883	134.5	8.7	818	1	NTRK2_CHICK	Q91987_gallus galli	956	132	8.5	508	2	Q8BUJ5_MOUSE	Q8BUJ5_mus musculus
884	134.5	8.7	904	2	Q7PME2_ANOGA	Q7PME2_anopheles g	957	132	8.5	627	2	Q5RDU0_PONPY	Q5RDU0_pongo pygma
885	134.5	8.7	949	1	MAMC1_MOUSE	P60755_mus musculus	958	132	8.5	707	2	Q5BJU3_MOUSE	Q5BJU3_mus musculus
886	134.5	8.7	1028	1	CNTN3_MOUSE	Q07409_mus musculus	959	132	8.5	743	2	Q6PIM7_HUMAN	Q6PIM7_homo sapien
887	134.5	8.7	1180	2	Q51S85_9PRIM	Q51S85_saimiri bol	960	132	8.5	947	1	MUSK_CHICK	Q8AXY6_gallus galli
888	134.5	8.7	1880	2	Q18465_HIRME	Q18465_hirudo medi	961	132	8.5	1018	1	CNTN1_BOVIN	Q28106_bos taurus
889	134.5	8.7	2154	2	Q8WZ51_HUMAN	Q8WZ51_homo sapien	962	132	8.5	1018	1	CNTN1_HUMAN	Q12860_homo sapien
890	134.5	8.7	2200	2	Q7YRFE_CANFA	Q7YRFE_canis famli	963	132	8.5	1019	2	Q8BUK6_MOUSE	Q8BUK6_mus musculus
891	134	8.7	308	2	Q5WRG1_SHEEP	Q5WRG1_ovis aries	964	132	8.5	1166	2	Q9QVNA_9MURI	Q9QVNA_rattus sp.
892	134	8.7	334	2	Q02870_CHICK	Q02870_gallus galli	965	132	8.5	1194	2	Q6PW35_RAT	Q6PW35_rattus norv
893	134	8.7	344	2	Q6B014_HUMAN	Q6B014_homo sapien	966	132	8.5	1197	2	Q6PW38_RAT	Q6PW38_rattus norv
894	134	8.7	351	2	Q8TFU3_BRARE	Q8TFU3_brachydantio	967	132	8.5	1198	2	Q6PW37_RAT	Q6PW37_rattus norv
895	134	8.7	351	2	Q7SY58_BRARE	Q7SY58_brachydantio	968	132	8.5	1206	2	Q6PW36_RAT	Q6PW36_rattus norv
896	134	8.7	458	2	Q63093_RAT	Q63093_rattus norv	969	132	8.5	1209	2	Q6PW39_RAT	Q6PW39_rattus norv
897	134	8.7	484	2	Q26475_SCHAM	Q26475_schistocerc	970	132	8.5	1214	1	NRCAM_RAT	P7686_rattus norv
898	134	8.7	628	1	LO_HUMAN	P50895_homo sapien	971	132	8.5	1299	2	Q6PW34_RAT	Q6PW34_rattus norv
899	134	8.7	919	1	UNC5_CAEEL	Q26261_cenorhabdi	972	131.5	8.5	263	2	Q7TPW5_MOUSE	Q7TPW5_mus musculus
900	134	8.7	941	2	Q5J1R9_BRARE	Q5J1R9_brachydantio	973	131.5	8.5	417	1	PVR_HUMAN	P15151_homo sapien
901	134	8.7	1044	2	Q961W3_HUMAN	Q961W3_homo sapien	974	131.5	8.5	419	1	PSG4_HUMAN	Q00888_homo sapien
902	134	8.7	1077	2	Q5WM88_CAEBR	Q5WM88_cenorhabdi	975	131.5	8.5	731	2	Q8CFK8_MOUSE	Q8CFK8_mus musculus
903	134	8.7	2095	2	Q4RYE5_TETNG	Q4RYE5_tetractodon n	976	131.5	8.5	733	2	Q60830_MOUSE	Q60830_mus musculus
904	133.5	8.6	241	2	Q4T4Z6_TETNG	Q4T4Z6_tetractodon n	977	131.5	8.5	764	2	Q5RDC2_PONPY	Q5RDC2_pongo pygma
905	133.5	8.6	308	2	Q8UUG3_ICTPU	Q8UUG3_ictaluron p	978	131.5	8.5	764	2	Q5RA58_PONPY	Q5RA58_pongo pygma
906	133.5	8.6	330	1	EMB_MOUSE	P21995_mus musculus	979	131.5	8.5	789	1	KIRRI_RAT	Q6X936_rattus norv
907	133.5	8.6	331	2	Q63239_RAT	Q63239_rattus norv	980	131.5	8.5	820	2	Q8CTM9_MOUSE	Q8CTM9_mus musculus

981	131.5	8.5	822	1	FGRL1_MOUSE	P16092 mus musculus	1054	129.5	8.4	510	2	Q9JLB8_MOUSE	Q9JLB8 mus musculus
982	131.5	8.5	822	2	Q60818_MOUSE	Q60818 mus musculus	1055	129.5	8.4	731	2	Q5BJG2_HUMAN	Q5BJG2 mus sapien
983	131.5	8.5	1047	2	Q4RGCT_TETNG	Q4RGCT tetradodon n	1056	129.5	8.4	740	1	PECA1_FIG	PECA1 fig
984	131.5	8.5	1266	1	NGCA_CHICK	NGC1966 gallus galli	1057	129.5	8.4	750	2	Q646H5_CAEBL	Q646H5 caenorhabd1
985	131.5	8.5	1335	2	Q610C7_CAEBR	Q610C7 caenorhabd1	1058	129.5	8.4	785	2	Q5XG39_XENLA	Q5XG39 xenopus lae
986	131.5	8.5	2029	1	LAR_DROME	P16621 drosophila	1059	129.5	8.4	797	2	Q52V40_BRAFL	Q52V40 brachylobo
987	131.5	8.5	2057	2	Q4T2N4_TETNG	Q4T2N4 tetradodon n	1060	129.5	8.4	814	2	Q59H40_HUMAN	Q59H40 homo sapien
988	131	8.5	226	2	Q8N440_TETNG	Q8N440 homo sapien	1061	129.5	8.4	822	1	FGFR1_HUMAN	P11362 homo sapien
989	131	8.5	321	2	Q5MRG0_SHEEP	Q5MRG0 ovis aries	1062	129.5	8.4	822	2	Q91288_PLEWA	Q91288 pleurodeles
990	131	8.5	352	2	Q61349_MOUSE	Q61349 mus musculus	1063	129.5	8.4	874	2	Q9Y166_BRAE	Q9Y166 brachydanio
991	131	8.5	350	1	NEGR1_HUMAN	Q723b1 homo sapien	1064	129.5	8.4	1073	2	Q9TX18_CAEBL	Q9TX18 caenorhabd1
992	131	8.5	354	2	Q5VT21_HUMAN	Q5VT21 homo sapien	1065	129.5	8.4	1073	2	Q9M1T8_DROME	Q9M1T8 drosophila
993	131	8.5	354	2	Q5R412_PONPY	Q5R412 pongo pygma	1066	129.5	8.4	1098	2	Q691D6_DROME	Q691D6 drosophila
994	131	8.5	362	2	Q9JH01_RAT	Q9JH01 rattus norv	1067	129.5	8.4	1343	1	VGFR2_RAT	Q08775 rattus norv
995	131	8.5	412	2	Q5U334_RAT	Q5U334 rattus norv	1068	129.5	8.4	1906	2	Q801W8_BRAE	Q801W8 brachydanio
996	131	8.5	412	2	Q63611_RAT	Q63611 rattus norv	1069	129	8.4	191	2	Q9CWD9_MOUSE	Q9CWD9 m mus muscu
997	131	8.5	412	2	Q9A1E1_RAT	Q9A1E1 rattus norv	1070	129	8.4	266	1	Q566X2_BRAE	Q566X2 brachydanio
998	131	8.5	463	2	Q4VAH7_MOUSE	Q4VAH7 mus musculus	1071	129	8.4	336	1	CD226_MACMU	Q18966 macaca mula
999	131	8.5	500	2	Q9XZB7_MOUSE	Q9XZB7 mus musculus	1072	129	8.4	393	2	Q55727_HUMAN	Q55727 homo sapien
1000	131	8.5	500	2	Q9WZ60_DROME	Q9WZ60 drosophila	1073	129	8.4	459	2	Q86X91_HUMAN	Q86X91 homo sapien
1001	131	8.5	501	2	Q4SZCS_TETNG	Q4SZCS tetradodon n	1074	129	8.4	510	2	Q801V8_BRAE	Q801V8 brachydanio
1002	131	8.5	636	2	Q22040_CAEBL	Q22040 caenorhabd1	1075	129	8.4	542	2	Q8NHN5_HUMAN	Q8NHN5 homo sapien
1003	131	8.5	831	2	Q71SY9_CHICK	Q71SY9 gallus galli	1076	129	8.4	802	2	Q95M13_BOVIN	Q95M13 bos taurus
1004	131	8.5	1012	2	Q4SM91_TETNG	Q4SM91 tetradodon n	1077	129	8.4	816	2	Q91285_PLEWA	Q91285 pleurodeles
1005	131	8.5	1276	2	Q90X22_BRAE	Q90X22 brachydanio	1078	129	8.4	1014	2	Q8NFA6_HUMAN	Q8NFA6 homo sapien
1006	131	8.5	1944	2	Q695U3_BRAE	Q695U3 brachydanio	1079	129	8.4	1197	2	Q4RVM1_TETNG	Q4RVM1 tetradodon n
1007	130.5	8.5	173	2	Q7PSS8_ANOGA	Q7PSS8 anopheles g	1080	129	8.4	1357	2	Q5MD89_BRAE	Q5MD89 brachydanio
1008	130.5	8.5	238	2	Q20339_CAEBL	Q20339 caenorhabd1	1081	129	8.4	1357	2	Q5G1T2_BRAE	Q5G1T2 brachydanio
1009	130.5	8.5	313	2	Q9U964_GEOCY	Q9U964 geodia cydo	1082	129	8.4	1427	2	Q91562_XENLA	Q91562 xenopus lae
1010	130.5	8.5	383	2	Q18431_GEOCY	Q18431 geodia cydo	1083	129	8.4	2164	2	Q91A99_CHICK	Q91A99 gallus galli
1011	130.5	8.5	393	1	ILIR2_CERAE	Q29612 ceratopithec	1084	129	8.4	3100	2	Q7KYN5_HUMAN	Q7KYN5 homo sapien
1012	130.5	8.5	424	1	PSG10_HUMAN	Q05235 homo sapien	1085	129	8.4	4650	2	Q15598_HUMAN	Q15598 homo sapien
1013	130.5	8.5	435	1	PSG6_HUMAN	Q00889 homo sapien	1086	129	8.4	5505	2	Q4RU89_TETNG	Q4RU89 tetradodon n
1014	130.5	8.5	505	2	Q9U965_GEOCY	Q9U965 geodia cydo	1087	129	8.4	18412	2	Q7Z261_BRAE	Q7Z261 brachydanio
1015	130.5	8.5	549	2	Q9D006_MOUSE	Q9D006 mus musculus	1088	128.5	8.3	226	2	Q4T419_TETNG	Q4T419 tetradodon n
1016	130.5	8.5	562	2	Q6YNR7_BRAE	Q6YNR7 brachydanio	1089	128.5	8.3	233	2	Q96169_HUMAN	Q96169 homo sapien
1017	130.5	8.5	593	2	Q5W0P9_HUMAN	Q5W0P9 homo sapien	1090	128.5	8.3	322	1	ICOSL_MOUSE	Q9J168 mus musculus
1018	130.5	8.5	757	1	KTRR1_HUMAN	Q96J84 homo sapien	1091	128.5	8.3	322	2	Q544C7_MOUSE	Q544C7 mus musculus
1019	130.5	8.5	757	1	Q5W0F8_HUMAN	Q5W0F8 homo sapien	1092	128.5	8.3	341	2	Q503N3_BRAE	Q503N3 brachydanio
1020	130.5	8.5	814	2	Q9VNP2_DROME	Q9VNP2 drosophila	1093	128.5	8.3	348	1	NEGR1_RAT	Q9Z018 rattus norv
1021	130.5	8.5	877	2	Q9GSH3_HALRO	Q9GSH3 halocynthia	1094	128.5	8.3	385	1	BASI_HUMAN	Q9Z018 rattus norv
1022	130.5	8.5	1011	2	Q24273_DROME	Q24273 drosophila	1095	128.5	8.3	395	2	Q5SKX1_HUMAN	Q5SKX1 h baigrin p
1023	130.5	8.5	1033	2	Q4SBZ7_TETNG	Q4SBZ7 tetradodon n	1096	128.5	8.3	413	2	Q4HIG8_SAMCR	Q4HIG8 samla cynth
1024	130	8.4	166	2	Q15226_HUMAN	Q15226 homo sapien	1097	128.5	8.3	419	2	Q6P520_HUMAN	Q6P520 homo sapien
1025	130	8.4	229	2	Q9R121_RAT	Q9R121 rattus norv	1098	128.5	8.3	549	2	Q9JUB9_MOUSE	Q9JUB9 mus musculus
1026	130	8.4	237	2	Q8BTP3_MOUSE	Q8BTP3 mus musculus	1099	128.5	8.3	574	2	Q58EG3_BRAE	Q58EG3 brachydanio
1027	130	8.4	330	2	Q90Z88_BRAE	Q90Z88 brachydanio	1100	128.5	8.3	797	2	Q52V39_BRAFL	Q52V39 brachylobo
1028	130	8.4	509	2	Q6P618_MOUSE	Q6P618 mus musculus	1101	128.5	8.3	1343	2	Q5POU0_RAT	Q5POU0 rattus norv
1029	130	8.4	529	1	FGRL1_MOUSE	Q91V87 mus musculus	1102	128.5	8.3	2935	2	Q721Y4_DROME	Q721Y4 drosophila
1030	130	8.4	888	2	Q4VBK2_BRAE	Q4VBK2 brachydanio	1103	128.5	8.3	2946	2	Q9W053_DROME	Q9W053 drosophila
1031	130	8.4	1019	2	Q9Y6L9_HUMAN	Q9Y6L9 homo sapien	1104	128	8.3	243	2	Q611Y6_CAEBR	Q611Y6 caenorhabd1
1032	130	8.4	1106	2	Q8WX93_HUMAN	Q8WX93 homo sapien	1105	128	8.3	331	2	Q91B01_9PERC	Q91B01 spherooides
1033	130	8.4	1228	2	Q8MRA3_DROME	Q8MRA3 drosophila	1106	128	8.3	333	2	Q61RX2_HUMAN	Q61RX2 homo sapien
1034	130	8.4	1235	2	Q9V787_DROME	Q9V787 drosophila	1107	128	8.3	422	2	Q96FP3_HUMAN	Q96FP3 homo sapien
1035	130	8.4	1235	2	Q86BD5_DROME	Q86BD5 drosophila	1108	128	8.3	423	2	Q8BU57_MOUSE	Q8BU57 mus musculus
1036	130	8.4	1252	2	Q9EQS9_MOUSE	Q9EQS9 mus musculus	1109	128	8.3	506	1	SHPS1_BOVIN	Q46631 bos taurus
1037	130	8.4	1253	2	Q9EQS8_MOUSE	Q9EQS8 mus musculus	1110	128	8.3	542	2	Q5USW7_MOUSE	Q5USW7 mus musculus
1038	130	8.4	1409	2	Q801M2_BRAE	Q801M2 brachydanio	1111	128	8.3	707	2	Q9TT07_CANFA	Q9TT07 canis famli
1039	130	8.4	1409	2	Q801M2_BRAE	Q801M2 brachydanio	1112	128	8.3	739	2	Q60NV9_CAEBR	Q60NV9 caenorhabd1
1040	130	8.4	1428	2	Q8AV67_BRAE	Q8AV67 brachydanio	1113	128	8.3	823	1	CEK3_CHICK	P18451 gallus galli
1041	130	8.4	2200	1	LAR_CAEBL	Q9PM68 caenorhabd1	1114	128	8.3	1032	1	CNT1A_BRAE	Q8AX44 brachydanio
1042	129.5	8.4	151	2	Q4THV8_TETNG	Q4THV8 tetradodon n	1115	128	8.3	1253	2	Q4SCT8_TETNG	Q4SCT8 tetradodon n
1043	129.5	8.4	275	2	Q6PH44_BRAE	Q6PH44 brachydanio	1116	128	8.3	1253	2	Q6ZP22_MOUSE	Q6ZP22 mus musculus
1044	129.5	8.4	306	1	CD80_MOUSE	Q00609 mus musculus	1117	128	8.3	2176	2	Q6V4S5_MOUSE	Q6V4S5 mus musculus
1045	129.5	8.4	306	2	Q549R2_MOUSE	Q549R2 mus musculus	1118	127.5	8.3	262	2	Q80T70_MOUSE	Q80T70 mus musculus
1046	129.5	8.4	323	2	Q5U198_DROME	Q5U198 drosophila	1119	127.5	8.3	276	2	Q5MKL4_HUMAN	Q5MKL4 homo sapien
1047	129.5	8.4	338	2	Q7Z3W6_HUMAN	Q7Z3W6 homo sapien	1120	127.5	8.3	323	2	Q7ORAT_ANOGA	Q7ORAT anopheles g
1048	129.5	8.4	338	2	Q5R7J4_HUMAN	Q5R7J4 homo sapien	1121	127.5	8.3	348	1	NEGR1_MOUSE	Q80Z44 mus musculus
1049	129.5	8.4	398	2	Q7Z3B9_HUMAN	Q7Z3B9 homo sapien	1122	127.5	8.3	388	2	Q8NRZ8_HUMAN	Q8NRZ8 homo sapien
1050	129.5	8.4	403	2	Q9N2H5_HORSE	Q9N2H5 equus caball	1123	127.5	8.3	422	2	Q8WR61_LYMDI	Q8WR61 lymphatic d
1051	129.5	8.4	403	2	Q4SFV2_TETNG	Q4SFV2 tetradodon n	1124	127.5	8.3	487	1	FGRL1_CHICK	Q7C212 gallus galli
1052	129.5	8.4	438	2	Q9JLB7_MOUSE	Q9JLB7 mus musculus	1125	127.5	8.3	898	1	FAST_SCHAM	P22648 schistocerc
1053	129.5	8.4	466	2	Q4VMT2_PIPPI	Q4VMT2 xenopus sp.	1126	127.5	8.3	1040	2	Q9W6T5_BRAE	Q9W6T5 brachydanio

1127	127.5	8.3	1166	1	PGFRB_HUMAN	P09619	homo sapien	1200	125.5	8.1	1028	1	CNTN3_RAT	Q62682	rattus norv
1128	127.5	8.3	1157	1	L1CAL_BRARE	Q90478	brachydanio	1201	125.5	8.1	1055	1	O61Y10_CAEBR	Q61Y10	caenorhabdi
1129	127.5	8.3	1159	2	Q9W15_BRARE	Q6U715	brachydanio	1202	125.5	8.1	1263	2	Q7Z3B7_HUMAN	Q7Z3B7	homo sapien
1130	127.5	8.3	1304	2	Q9VB5_DROME	Q9VB5	DROME	1203	125.5	8.1	1284	1	NRCAM_CHICK	P35331	gallus galli
1131	127	8.2	103	2	Q8NN6_HUMAN	Q8NN6	homo sapien	1204	125	8.1	234	2	O5C242_HUMAN	O5C242	homo sapien
1132	127	8.2	271	2	Q4S717_TETNG	Q4S717	tetradodon n	1205	125	8.1	235	2	Q75226_HUMAN	Q75226	homo sapien
1133	127	8.2	276	2	Q4SF97_TETNG	Q4SF97	tetradodon n	1206	125	8.1	287	2	Q9QW80_MUORI	Q9QW80	mus sp. fib
1134	127	8.2	353	2	Q63242_RAT	Q63242	rattus norv	1207	125	8.1	360	2	Q8BJ10_MOUSE	Q8BJ10	mus musculus
1135	127	8.2	413	2	Q9VAR6_DROME	Q9VAR6	DROSOPHILA	1208	125	8.1	376	2	Q9QW78_MUORI	Q9QW78	mus sp. fib
1136	127	8.2	416	1	RAGE_BOVIN	Q28173	bos taurus	1209	125	8.1	403	2	Q8HY15_LEMCA	Q8HY15	lemur catrea
1137	127	8.2	459	2	Q4RS1_TETNG	Q4RS1	tetradodon n	1210	125	8.1	448	2	Q9JH17_RAT	Q9JH17	rattus norv
1138	127	8.2	461	2	Q4RPF6_TETNG	Q4RPF6	tetradodon n	1211	125	8.1	495	2	Q4TA17_TETNG	Q4TA17	tetradodon n
1139	127	8.2	515	2	Q96RE0_HUMAN	Q96RE0	homo sapien	1212	125	8.1	530	1	PRR2_MOUSE	P34507	mus musculus
1140	127	8.2	515	2	Q96P05_HUMAN	Q96P05	homo sapien	1213	125	8.1	603	2	Q4SLP0_TETNG	Q4SLP0	tetradodon n
1141	127	8.2	523	2	Q80ZE2_MOUSE	Q80ZE2	mus musculus	1214	125	8.1	626	2	Q4SM56_TETNG	Q4SM56	tetradodon n
1142	127	8.2	569	1	SIGL2_MOUSE	Q92003	mus musculus	1215	125	8.1	709	2	Q4KL27_RAT	Q4KL27	rattus norv
1143	127	8.2	686	1	IRPL2_HUMAN	Q9NP60	h x-linked	1216	125	8.1	766	2	Q7Q057_ANOGA	Q7Q057	anopheles g
1144	127	8.2	686	2	Q5H9L5_HUMAN	Q5H919	homo sapien	1217	125	8.1	766	2	Q7Q057_ANOGA	Q7Q057	anopheles g
1145	127	8.2	709	1	CEAM3_RAT	Q63181	rattus norv	1218	125	8.1	775	2	Q97754_RABIT	Q97754	oryctolagus
1146	127	8.2	800	2	Q918X3_BRARE	Q918X3	brachydanio	1219	125	8.1	937	2	Q5WM68_CAEBR	Q5WM68	caenorhabdi
1147	127	8.2	810	2	Q9SP96_XENLA	Q9SP96	xenopus lae	1220	125	8.1	1072	2	Q8T104_BOOMO	Q8T104	boomo
1148	127	8.2	873	2	Q98949_CHICK	Q98949	gallus galli	1221	125	8.1	1802	2	Q28633_RABIT	Q28633	oryctolagus
1149	127	8.2	1009	2	Q93250_XENLA	Q93250	xenopus lae	1222	125	8.1	4001	2	Q9N2P7_DROME	Q9N2P7	drosophila
1150	127	8.2	1153	2	Q4RHWA_TETNG	Q4RHWA	tetradodon n	1223	124.5	8.1	235	2	Q9N070_CANFA	Q9N070	canis famill
1151	127	8.2	14816	2	Q8T103_BOOMO	Q8T103	boombx mori	1224	124.5	8.1	235	2	Q9TQ58_CANFA	Q9TQ58	canis famill
1152	126.5	8.2	272	2	Q8R1N5_HUMAN	Q8R1N5	mus musculus	1225	124.5	8.1	284	2	Q9GLJ3_BOVIN	Q9GLJ3	bos taurus
1153	126.5	8.2	311	2	Q6DN73_HUMAN	Q6DN73	homo sapien	1226	124.5	8.1	304	2	Q9TQX1_CANFA	Q9TQX1	canis famill
1154	126.5	8.2	446	2	Q63337_RAT	Q63337	rattus norv	1227	124.5	8.1	325	2	Q8UWJ3_ICTPU	Q8UWJ3	icetalurus p
1155	126.5	8.2	513	2	Q9D6N4_MOUSE	Q9D6N4	mus musculus	1228	124.5	8.1	327	1	EMB_HUMAN	Q6Cpb8	homo sapien
1156	126.5	8.2	530	2	Q53H63_HUMAN	Q53H63	homo sapien	1229	124.5	8.1	359	2	Q4KL24_XENLA	Q4KL24	xenopus lae
1157	126.5	8.2	824	2	Q90749_CHICK	Q90749	gallus galli	1230	124.5	8.1	413	2	Q26438_HYACE	Q26438	hyalophora
1158	126.5	8.2	966	2	Q8UVA9_FUGRU	Q8UVA9	fugu rubrip	1231	124.5	8.1	698	2	O5NTN5_ANOGA	O5NTN5	anopheles g
1159	126.5	8.2	1232	2	Q90284_CARAV	Q90284	caerassius a	1232	124.5	8.1	769	1	PGFR1_RAT	P21804	rattus norv
1160	126.5	8.2	1238	2	Q58OC3_XENLA	Q58OC3	xenopus lae	1233	124.5	8.1	819	1	PGFR1_CHICK	P21804	rattus norv
1161	126.5	8.2	1250	2	Q62404_CAEBR	Q62404	caenorhabdi	1234	124.5	8.1	848	2	Q7QCUC_ANOGA	Q7QCUC	anopheles g
1162	126.5	8.2	1445	2	Q63155_RAT	Q63155	rattus norv	1235	124.5	8.1	886	2	Q9VM64_DROME	Q9VM64	drosophila
1163	126.5	8.2	1447	1	DOC_HUMAN	Q4FZV9	xenopus lae	1236	124.5	8.1	917	1	ICAMS_MOUSE	Q60625	mus musculus
1164	126	8.2	270	2	Q4FZV9_XENLA	Q4FZV9	xenopus lae	1237	124.5	8.1	954	2	Q7PVU4_ANOGA	Q7PVU4	anopheles g
1165	126	8.2	275	2	Q55107_MOUSE	Q55107	mus musculus	1238	124.5	8.1	1007	1	ROBO4_HUMAN	Q8PW75	homo sapien
1166	126	8.2	332	2	Q9VAV8_DROME	Q9VAV8	DROSOPHILA	1239	124.5	8.1	1075	2	Q8TPZ2_METAC	Q8TPZ2	methanogarr
1167	126	8.2	336	2	Q4S1B2_TETNG	Q4S1B2	tetradodon n	1240	124.5	8.1	2217	2	Q8AVS7_CHICK	Q8AVS7	gallus galli
1168	126	8.2	359	1	BASI_MOUSE	P18572	mus musculus	1241	124.5	8.1	4203	2	Q96552_CHICK	Q96552	caenorhabdi
1169	126	8.2	475	2	Q62664_RAT	Q62664	rattus norv	1242	124.5	8.1	4219	2	Q9L871_CAEBL	Q9L871	caenorhabdi
1170	126	8.2	529	1	FGRL1_RAT	Q7QML4	rattus norv	1243	124.5	8.1	4250	2	O5PY59_CAEBL	O5PY59	caenorhabdi
1171	126	8.2	539	2	Q4VBP8_RAT	Q4VBP8	rattus norv	1244	124.5	8.1	4447	2	Q8MXK8_CAEBL	Q8MXK8	caenorhabdi
1172	126	8.2	673	2	Q6MZW2_HUMAN	Q6MZW2	homo sapien	1245	124.5	8.1	4467	2	Q8MXK8_CAEBL	Q8MXK8	caenorhabdi
1173	126	8.2	708	1	KIRK2_HUMAN	Q6UW16	homo sapien	1246	124.5	8.1	4889	2	Q9TXK2_CAEBL	Q9TXK2	caenorhabdi
1174	126	8.2	881	2	Q965M2_CAEBL	Q965M2	caenorhabdi	1247	124	8.0	243	2	O61A22_HYMAN	O61A22	homo sapien
1175	126	8.2	941	2	Q4SMD8_TETNG	Q4SMD8	tetradodon n	1248	124	8.0	316	2	O5SNN7_BRARE	O5SNN7	brachydanio
1176	126	8.2	1059	1	CNTN5_RAT	P97527	rattus norv	1249	125	8.0	336	2	Q46551_PPRIM	Q46551	hylobates s
1177	126	8.2	1252	2	Q9JILI_MOUSE	Q9JILI	mus musculus	1250	124	8.0	380	2	O5T2D2_HUMAN	O5T2D2	homo sapien
1178	126	8.2	1282	2	Q4RHM3_TETNG	Q4RHM3	tetradodon n	1251	124	8.0	388	1	BASI_RAT	P26453	rattus norv
1179	126	8.2	1357	2	Q8QHL3_CHICK	Q8QHL3	gallus galli	1252	124	8.0	391	2	Q4S871_TETNG	Q4S871	tetradodon n
1180	126	8.2	1356	1	VGFR2_HUMAN	P35968	homo sapien	1253	124	8.0	452	2	O5XKT3_BRARE	O5XKT3	brachydanio
1181	126	8.2	1451	2	O5SEB0_HUMAN	O5SEB0	homo sapien	1254	124	8.0	457	2	Q960D1_DROME	Q960D1	drosophila
1182	126	8.2	4736	2	Q9NL88_DROME	Q9NL88	DROSOPHILA	1255	124	8.0	468	2	Q9XY08_BOOMO	Q9XY08	boombx mori
1183	126	8.2	4736	2	Q9W055_DROME	Q9W055	DROSOPHILA	1256	124	8.0	504	2	Q98923_CHICK	Q98923	gallus galli
1184	125.5	8.1	140	2	Q4S488_TETNG	Q4S488	tetradodon n	1257	124	8.0	577	2	Q9D221_MOUSE	Q9D221	mus musculus
1185	125.5	8.1	337	2	Q8UVZ9_HUMAN	Q8UVZ9	brachydanio	1258	124	8.0	584	2	Q98921_CHICK	Q98921	gallus galli
1186	125.5	8.1	337	2	Q90287_BRARE	Q90287	brachydanio	1259	124	8.0	626	2	Q98922_CHICK	Q98922	gallus galli
1187	125.5	8.1	338	1	ILIR2_HUMAN	P79730	homo sapien	1260	124	8.0	696	1	IRPL1_PONPY	Q79419	pongo pygma
1188	125.5	8.1	400	2	O8HY16_CEBAP	O8HY16	cebu sapell	1261	124	8.0	949	2	O8IGN3_DROME	O8IGN3	drosophila
1189	125.5	8.1	419	1	PGS7_HUMAN	Q33046	homo sapien	1262	124	8.0	1389	2	Q4VAF1_MOUSE	Q4VAF1	mus musculus
1190	125.5	8.1	439	2	O57319_CHICK	O57344	gallus galli	1263	124	8.0	1400	2	Q7P94_ANOGA	Q7P94	anopheles g
1191	125.5	8.1	460	2	Q8WU24_PANTR	Q8WU24	pan troglod	1264	124	8.0	1958	2	Q4SE42_TETNG	Q4SE42	tetradodon n
1192	125.5	8.1	606	2	Q9BS57_MOUSE	Q9BS57	mus musculus	1265	123.5	8.0	182	2	Q15232_HUMAN	Q15232	homo sapien
1193	125.5	8.1	683	2	O5TJY6_ANOGA	O5TJY6	anopheles g	1266	123.5	8.0	258	2	O5VZT8_HUMAN	O5VZT8	homo sapien
1194	125.5	8.1	737	2	Q9JUI0_RAT	Q9JUI0	rattus norv	1267	123.5	8.0	262	2	O8NA19_HUMAN	O8NA19	homo sapien
1195	125.5	8.1	737	2	Q965M3_CAEBL	Q965M3	caenorhabdi	1268	123.5	8.0	312	2	O66KX0_XENLA	O66KX0	xenopus lae
1196	125.5	8.1	743	2	Q6R6B2_SCARD	Q6R6B2	vicatrix phag	1269	123.5	8.0	375	1	TAMU1_MOUSE	Q8U019	mus musculus
1197	125.5	8.1	747	2	Q4H3K6_CTOIN	Q4H3K6	ctona inter	1270	123.5	8.0	388	2	Q8R464_MOUSE	Q8R464	mus musculus
1198	125.5	8.1	789	1	KIRI1_MOUSE	Q8U068	mus musculus	1271	123.5	8.0	413	1	HEMO_HYACE	P25033	hyalophora
1199	125.5	8.1	821	1	PGFR2_HUMAN	P21802	homo sapien	1272	123.5	8.0	503	1	SHPS1_HUMAN	P25034	h tyrosine-

1273	123.5	8.0	555	1	CD166_CARAU	090304 carassius a	1346	121.5	7.9	336	2	0961T8_DROME	0961E8 drosophila
1274	123.5	8.0	662	2	08M1Z6_PANTR	08M1Z6 pan troglod	1347	121.5	7.9	357	2	061238_RAT	061238 rattus norv
1275	123.5	8.0	669	2	06B515_POEGU	06B515 poephila gu	1348	121.5	7.9	404	1	RAGE_HUMAN	015109 homo sapien
1276	123.5	8.0	796	2	091287_PLEWA	091287 pleurodeles	1349	121.5	7.9	635	2	04S1S8_TETNG	04S1S8 tetraodon n
1277	123.5	8.0	885	2	08N237_HUMAN	08N237 homo sapien	1350	121.5	7.9	700	1	K1R4Z_MOUSE	07E1U7 mus musculu
1278	123.5	8.0	1000	2	04TBR4_TETNG	04TBR4 tetraodon n	1351	121.5	7.9	700	1	K1R4Z_MOUSE	0184Z3 geoccy
1279	123.5	8.0	1209	2	P70232_MOUSE	P70232 mus musculu	1352	121.5	7.9	733	2	09QZM7_MOUSE	09QZM7 mus musculu
1280	123	8.0	231	2	08WY6_HUMAN	08WY6 homo sapien	1353	121.5	7.9	782	2	09TTZ3_RABIT	09TTZ3 corycolagus
1281	123	8.0	249	1	BASI_CRICR	09P9A3 cisticulus	1354	121.5	7.9	782	2	0615G3_MOUSE	0615G3 mus musculu
1282	123	8.0	307	2	094431_CIOIN	094431 ciona intes	1355	121.5	7.9	893	2	05TN14_ANOGA	05TN14 xenopus lae
1283	123	8.0	351	2	06WBE2_BRALA	06WBE2 branchiocto	1356	121.5	7.9	1177	2	06GQBI_XENLA	06GQBI xenopus lae
1284	123	8.0	380	2	09HBE9_HUMAN	09HBE9 homo sapien	1357	121.5	7.9	1447	1	DCC_MOUSE	P70211 mus musculu
1285	123	8.0	381	2	09Y4A4_HUMAN	09Y4A4 homo sapien	1358	121.5	7.9	1471	2	018245_CAEEL	018245 caenorhabd
1286	123	8.0	530	2	04RTW9_TETNG	04RTW9 tetraodon n	1359	121	7.8	265	2	061XU3_RABIT	061XU3 corycolagus
1287	123	8.0	812	1	RGFR1_XENLA	P22182 xenopus lae	1360	121	7.8	275	1	0055_FDPGP	P21975 fowlopx vir
1288	123	8.0	812	1	08N612_HUMAN	08N612 homo sapien	1361	121	7.8	275	2	070H56_FOWPV	070H56 fowlopx vir
1289	123	8.0	924	2	08TAM9_HUMAN	08TAM9 homo sapien	1362	121	7.8	336	2	08UV73_BRARE	08UV73 brachydanio
1290	123	8.0	939	2	0967X6_DROME	0967X6 drosophila	1363	121	7.8	402	2	035444_MOUSE	035444 mus musculu
1291	123	8.0	949	2	09VWZ7_DROME	09VWZ7 drosophila	1364	121	7.8	446	2	061236_RAT	061236 rattus norv
1292	122.5	7.9	242	2	046604_PIG	046604 sus scrofa	1365	121	7.8	475	2	04VB15_RAT	04VB15 rattus norv
1293	122.5	7.9	294	2	08K1Z5_MOUSE	08K1Z5 mus musculu	1366	121	7.8	695	1	IRPL1_MOUSE	P59823 mus musculu
1294	122.5	7.9	299	1	CD80_RABIT	P42070 corycolagus	1367	121	7.8	696	1	IRPL1_MOUSE	P59824 rattus norv
1295	122.5	7.9	306	2	06GMV6_HUMAN	06GMV6 homo sapien	1368	121	7.8	775	1	06PF50_XENLA	06PF50 xenopus lae
1296	122.5	7.9	314	2	05RDC1_PONPY	05RDC1 pongo pygma	1369	121	7.8	822	2	09QVU7_MURU	09QVU7 rattus sp.
1297	122.5	7.9	328	2	05R8B4_PONPY	05R8B4 pongo pygma	1370	121	7.8	844	2	05XG38_XENLA	05XG38 xenopus lae
1298	122.5	7.9	335	1	BSC2_HUMAN	P11465 homo sapien	1371	121	7.8	847	1	ESTL5_MOUSE	08bf52 mus musculu
1299	122.5	7.9	339	2	05VTE1_BRARE	05VTE1 brachydanio	1372	121	7.8	858	2	05VTT7_BRARE	05VTT7 brachydanio
1300	122.5	7.9	391	2	07T1U4_BRARE	07T1U4 brachydanio	1373	121	7.8	1437	2	044329_HIRME	044329 hirtudo medi
1301	122.5	7.9	424	2	08C6W0_MOUSE	08C6W0 mus musculu	1374	121	7.8	2007	2	04SM88_TETNG	04SM88 tetraodon n
1302	122.5	7.9	455	2	04RDF3_TETNG	04RDF3 tetraodon n	1375	121	7.8	3158	2	04TAD4_TETNG	04TAD4 tetraodon n
1303	122.5	7.9	606	2	09ESS8_RAT	09ESS8 rattus norv	1376	120.5	7.8	181	2	09DVU7_MOUSE	09DVU7 mus musculu
1304	122.5	7.9	646	1	MUC18_HUMAN	P41121 homo sapien	1377	120.5	7.8	217	2	06KGN0_GCAUD	06KGN0 bacterioph
1305	122.5	7.9	646	2	06PHR3_HUMAN	06PHR3 homo sapien	1378	120.5	7.8	227	2	0568D3_BRARE	0568D3 brachydanio
1306	122.5	7.9	646	2	09S812_HUMAN	09S812 homo sapien	1379	120.5	7.8	229	2	07Q5B0_ANOGA	07Q5B0 anopheles g
1307	122.5	7.9	646	2	08CANA_MOUSE	08CANA mus musculu	1380	120.5	7.8	265	2	04VJF0_DROME	04VJF0 drosophila
1308	122.5	7.9	732	2	05TR64_ANOGA	05TR64 anopheles g	1381	120.5	7.8	292	2	08W9J7_MERUN	08W9J7 meriones un
1309	122.5	7.9	1505	2	0706Z3_ANOGA	0706Z3 anopheles g	1382	120.5	7.8	294	2	06KGN1_GCAUD	06KGN1 bacterioph
1310	122.5	7.9	4824	2	095VM1_PROCL	095VM1 procambatus	1383	120.5	7.8	315	2	09VMB2_DROME	09VMB2 drosophila
1311	122.5	7.9	8625	2	086GD6_PROCL	086GD6 procambatus	1384	120.5	7.8	332	2	0684Q2_MOUSE	0684Q2 mus musculu
1312	122	7.9	171	2	06VZ10_CNPV	06VZ10 canarypox v	1385	120.5	7.8	335	2	08UUG6_BRARE	08UUG6 brachydanio
1313	122	7.9	243	1	CD48_HUMAN	P09326 homo sapien	1386	120.5	7.8	376	2	04VJF0_DROME	04VJF0 drosophila
1314	122	7.9	243	1	05U055_HUMAN	05U055 homo sapien	1387	120.5	7.8	483	2	07SX76_BRARE	07SX76 brachydanio
1315	122	7.9	272	2	06GT74_RAT	06GT74 rattus norv	1388	120.5	7.8	571	2	05M0G0_HUMAN	05M0G0 homo sapien
1316	122	7.9	279	2	09UD50_HUMAN	09UD50 homo sapien	1389	120.5	7.8	677	2	08OHL2_CHICK	08OHL2 gallus gall
1317	122	7.9	325	2	07Z6M3_HUMAN	07Z6M3 homo sapien	1390	120.5	7.8	827	2	06GNS5_XENLA	06GNS5 xenopus lae
1318	122	7.9	402	1	RAGE_RAT	063495 rattus norv	1391	120.5	7.8	1122	2	04SAB1_TETNG	04SAB1 tetraodon n
1319	122	7.9	402	1	06MG86_RAT	06MG86 rattus norv	1392	120.5	7.8	4194	2	061S53_CAEER	061S53 caenorhabd
1320	122	7.9	459	2	09JH16_RAT	09JH16 rattus norv	1393	120	7.8	248	2	06P0H1_BRARE	06P0H1 mus musculu
1321	122	7.9	477	2	05EAJ2_FUGRU	05EAJ2 fugu rubrip	1394	120	7.8	249	2	06XUV6_MOUSE	06XUV6 mus musculu
1322	122	7.9	537	2	07OEY8_ANOGA	07OEY8 anopheles g	1395	120	7.8	296	2	06LCB6_HUMAN	06LCB6 homo sapien
1323	122	7.9	557	2	04T6S0_TETNG	04T6S0 tetraodon n	1396	120	7.8	308	2	07Q863_ANOGA	07Q863 anopheles g
1324	122	7.9	571	2	05EG07_ICTPU	05EG07 ictalurus p	1397	120	7.8	337	2	091A24_SPERC	091A24 spheroctoides
1325	122	7.9	605	2	08TBU0_HUMAN	08TBU0 homo sapien	1398	120	7.8	355	2	04VB14_RAT	04VB14 rattus norv
1326	122	7.9	686	1	IRPL2_MOUSE	09E866 mus musculu	1399	120	7.8	600	2	08N7W7_HUMAN	08N7W7 homo sapien
1327	122	7.9	693	1	09UPU1_HUMAN	09UPU1 homo sapien	1400	120	7.8	795	2	05U418_XENLA	05U418 xenopus lae
1328	122	7.9	696	1	IRPL1_HUMAN	09GZU1 homo sapien	1401	120	7.8	939	2	09VB35_DROME	09VB35 drosophila
1329	122	7.9	696	1	IRPL1_PANTR	P60025 pan troglod	1402	120	7.8	976	2	05RID5_BRARE	05RID5 brachydanio
1330	122	7.9	696	1	05UYV0_HUMAN	05UYV0 homo sapien	1403	120	7.8	976	2	08UFR5_BRARE	08UFR5 brachydanio
1331	122	7.9	771	1	P1GR_MOUSE	070570 mus musculu	1404	120	7.8	976	2	09W755_BRARE	09W755 drosophila
1332	122	7.9	881	2	060UL6_CAEER	060UL6 caenorhabd	1405	120	7.8	1501	2	07KUX9_DROME	07KUX9 drosophila
1333	122	7.9	1150	2	08BSZ4_MOUSE	08BSZ4 mus musculu	1406	119.5	7.7	257	2	05S108_MOUSE	05S108 mus musculu
1334	122	7.9	1375	2	08M147_DROME	08M147 drosophila	1407	119.5	7.7	270	2	06XJY4_MOUSE	06XJY4 mus musculu
1335	122	7.9	1375	2	094537_DROME	094537 drosophila	1408	119.5	7.7	318	2	08AYZ8_VARV	08AYZ8 variola vir
1336	122	7.9	1526	2	094538_DROME	094538 drosophila	1409	119.5	7.7	343	2	05EG08_ICTPU	05EG08 ictalurus p
1337	122	7.9	1526	2	094538_DROME	094538 drosophila	1410	119.5	7.7	352	2	008266_HUMAN	008266 homo sapien
1338	121.5	7.9	189	2	015230_HUMAN	015230 homo sapien	1411	119.5	7.7	352	2	015403_HUMAN	015403 homo sapien
1339	121.5	7.9	199	2	08ND10_HUMAN	08ND10 homo sapien	1412	119.5	7.7	452	2	05MR11_CAEEL	05MR11 caenorhabd
1340	121.5	7.9	230	2	08QGS1_COTJA	08QGS1 cottomnix co	1413	119.5	7.7	464	2	04RGD6_TETNG	04RGD6 tetraodon n
1341	121.5	7.9	233	2	06NS96_HUMAN	06NS96 homo sapien	1414	119.5	7.7	556	2	05JYU7_HUMAN	05JYU7 homo sapien
1342	121.5	7.9	258	2	012811_HUMAN	012811 homo sapien	1415	119.5	7.7	834	2	052KGB_MOUSE	052KGB gallus gall
1343	121.5	7.9	298	2	08INK5_DROME	08INK5 drosophila	1416	119.5	7.7	960	1	KIT_CHICK	080156 gallus gall
1344	121.5	7.9	318	2	08BE16_VARV	08BE16 variola vir	1417	119.5	7.7	973	2	07QJ6_K_HUMAN	07QJ6 anopheles g
1345	121.5	7.9	318	2	09QNG4_VARV	09QNG4 variola vir	1418	119.5	7.7	1100	2	05RKM8_MOUSE	05RKM8 mus musculu

1419	119.5	7.7	10578	2	OBISF5_CAEEL	OBISF5 caenorhabdi
1420	119	7.7	413	2	O699P0_ANTPE	O699P0 anthracia p
1421	119	7.7	422	2	O86CT9_HELAM	O86CT9 hellicoverpa
1422	119	7.7	577	2	O80Y42_MOUSE	O80Y42 mus musculu
1423	119	7.7	620	2	O4SIC0_TETNG	O4SIC0 tetradon n
1424	119	7.7	675	2	O4S5Q4_TETNG	O4S5Q4 tetradon n
1425	119	7.7	880	2	O7KPO8_DROME	O7KPO8 drosophila
1426	119	7.7	1187	2	O589G5_CHICK	O589G5 gallus gall
1427	119	7.7	1390	1	CONT_DROME	O589G5 drosophila
1428	119	7.7	1390	2	O5B191_DROME	O5B191 drosophila
1429	118.5	7.7	1390	2	O8K1H8_MOUSE	O8K1H8 mus musculu
1430	118.5	7.7	269	2	O5RC22_PONPY	O5RC22 pongo pygma
1431	118.5	7.7	285	2	O5SNN8_BRARE	O5SNN8 brachydantio
1432	118.5	7.7	302	2	O5YJ10_SHEEP	O5YJ10 ovis aries
1433	118.5	7.7	352	2	O76697_CAEEL	O76697 caenorhabdi
1434	118.5	7.7	352	2	O76697_CAEEL	O76697 caenorhabdi
1435	118.5	7.7	379	2	O8BLK5_MOUSE	O8BLK5 mus musculu
1436	118.5	7.7	397	2	O8BFX8_MOUSE	O8BFX8 m mus muscu
1437	118.5	7.7	467	1	SIGL7_HUMAN	O9Y286 homo sapien
1438	118.5	7.7	528	2	P91670_DROME	P91670 drosophila
1439	118.5	7.7	538	2	O9NMQ7_HUMAN	O9NMQ7 homo sapien
1440	118.5	7.7	540	2	O8N0Z9_HUMAN	O8N0Z9 homo sapien
1441	118.5	7.7	545	2	O9VCT4_DROME	O9VCT4 drosophila
1442	118.5	7.7	582	2	O9SNT5_BOVIN	O9SNT5 bos taurus
1443	118.5	7.7	606	2	O6IRH8_RAT	O6IRH8 rattus norv
1444	118.5	7.7	697	1	SIG10_HUMAN	O961C7 homo sapien
1445	118.5	7.7	912	1	O7PUQ1_ANOGA	O7PUQ1 anopheles g
1446	118.5	7.7	912	1	ICAMS_RABIT	O287Q3 oryctolagus
1447	118.5	7.7	1187	2	O8MR45_CAEEL	O8MR45 caenorhabdi
1448	118.5	7.7	1195	2	O5TUS2_ANOGA	O5TUS2 anopheles g
1449	118.5	7.7	1228	2	O7QEI6_ANOGA	O7QEI6 anopheles g
1450	118.5	7.7	1464	2	O4SKS5_TETNG	O4SKS5 tetradon n
1451	118.5	7.7	2646	2	O4SLN8_TETNG	O4SLN8 tetradon n
1452	118	7.6	175	2	O4TGY2_TETNG	O4TGY2 tetradon n
1453	118	7.6	226	2	O7PUJ2_ANOGA	O7PUJ2 anopheles g
1454	118	7.6	233	2	O6PIW7_HUMAN	O6PIW7 homo sapien
1455	118	7.6	253	2	O17858_CAEEL	O17858 caenorhabdi
1456	118	7.6	270	2	O8BTN8_MOUSE	O8BTN8 mus musculu
1457	118	7.6	290	2	O5TNT8_ANOGA	O5TNT8 anopheles g
1458	118	7.6	321	2	O8IWO0_HUMAN	O8IWO0 homo sapien
1459	118	7.6	351	2	O7QOP8_ANOGA	O7QOP8 anopheles g
1460	118	7.6	381	2	O4SDA6_TETNG	O4SDA6 tetradon n
1461	118	7.6	385	2	O4SQV8_TETNG	O4SQV8 tetradon n
1462	118	7.6	421	2	O9NT99_HUMAN	O9NT99 homo sapien
1463	118	7.6	430	2	O58F20_HUMAN	O58F20 homo sapien
1464	118	7.6	553	2	O8WXT5_HUMAN	O8WXT5 homo sapien
1465	118	7.6	620	1	SMP_COTUA	O92154 coturnix co
1466	118	7.6	626	2	O90B80_CHICK	O90B80 gallus gall
1467	118	7.6	692	2	O4RV46_TETNG	O4RV46 tetradon n
1468	118	7.6	722	2	O6GNB3_XENLA	O6GNB3 xenopus lae
1469	118	7.6	769	2	O8N115_HUMAN	O8N115 homo sapien
1470	118	7.6	806	1	CEK2_CHICK	P18460 gallus gall
1471	118	7.6	806	1	FGFR3_HUMAN	P22607 homo sapien
1472	118	7.6	814	2	O91897_XENLA	O91897 xenopus lae
1473	118	7.6	838	2	O8WXT7_HUMAN	O8WXT7 homo sapien
1474	118	7.6	847	1	FSTL5_HUMAN	O8A475 homo sapien
1475	118	7.6	879	2	O59FL9_HUMAN	O59FL9 homo sapien
1476	118	7.6	924	1	ICAMS_HUMAN	O9UMF0 homo sapien
1477	118	7.6	1203	2	O4SRR2_TETNG	O4SRR2 tetradon n
1478	118	7.6	1415	2	O94155_CAEEL	O94155 caenorhabdi
1479	117.5	7.6	163	2	O9NVJ5_HUMAN	O9NVJ5 homo sapien
1480	117.5	7.6	391	2	O59EJ9_HUMAN	O59EJ9 homo sapien
1481	117.5	7.6	398	2	O9Y640_HUMAN	O9Y640 mus musculu
1482	117.5	7.6	403	1	RAGE_MOUSE	O62151 mus musculu
1483	117.5	7.6	467	2	O9LVT9_MOUSE	O9LVT9 mus musculu
1484	117.5	7.6	467	2	O8C6P2_MOUSE	O8C6P2 mus musculu
1485	117.5	7.6	538	1	PVR2_HUMAN	O92692 homo sapien
1486	117.5	7.6	556	1	ILRL1_HUMAN	O91638 homo sapien
1487	117.5	7.6	597	1	SIGL1_PANTR	O951H0 pan troglod
1488	117.5	7.6	603	2	O6PKF5_DROME	O6PKF5 drosophila
1489	117.5	7.6	743	2	O6P4F5_HUMAN	O6P4F5 homo sapien
1490	117.5	7.6	764	1	P1GR_HUMAN	P01833 homo sapien
1491	117.5	7.6	764	2	O81ZT7_HUMAN	O81ZT7 homo sapien

1492	117.5	7.6	764	2	O6BD81_HUMAN	O6BD81 homo sapien
1493	117.5	7.6	793	2	O4RY64_TETNG	O4RY64 tetradon n
1494	117.5	7.6	848	2	O25198_HYDAT	O25198 hydra atten
1495	117.5	7.6	1089	1	GFRA_HUMAN	O60T65 caenorhabdi
1496	117.5	7.6	1198	2	O60T65_CAEER	O60T65 caenorhabdi
1497	117.5	7.6	1240	1	NPASC_MOUSE	O810U3 mus musculu
1498	117.5	7.6	1251	2	O6ZOS4_MOUSE	O6ZOS4 mus musculu
1499	117.5	7.6	2343	2	O5TX11_ANOGA	O5TX11 anopheles g
1500	117.5	7.6	6710	2	O6ISF4_CAEER	O6ISF4 caenorhabdi

ALIGNMENTS					
RESULT 1	JAM1_HUMAN	STANDARD,	PRT,	299	AA.
AC	O9Y624:				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion molecule 1) (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet FII receptor).				
GN	Name=JAM1; Synonyms=JAM1, JCAM; ORNames=UHQ264/PRO301;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [MRNA].				
RX	MEBLINB=99323940; PubMed=10395639;				
RA	Ozaki H., Ishii K., Horituchi H., Arai H., Kawamoto T., Okawa K.,				
RA	Iwamatsu A., Kita T.;				
RT	"Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";				
RT	J. Immunol. 163:553-557(1999).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE [MRNA].				
RX	Submed=10753840;				
RA	Submed M.B., Sobocki T., Banerjee P., Weiss C., Rushbrook J.I.,				
RA	Norin A.U., Hartwig J., Salifu M.O., Markell M.S., Babinaka A.,				
RA	Ehrlich Y.H., Kornecki E.;				
RT	"Cloning of the human platelet FII receptor: a cell adhesion molecule member of the immunoglobulin superfamily involved in platelet aggregation.";				
RT	Blood 95:2600-2609(2000).				
RL	[3]				
RN	NUCLEOTIDE SEQUENCE [MRNA], AND SUBCELLULAR LOCATION.				
RP	Pubmed=11171323;				
RX	Naik U.P., Naik M.V., Eckfeld K., Martin-Deleon P., Spychnala J.;				
RT	"Characterization and chromosomal localization of JAM-1, a platelet receptor for a stimulatory monoclonal antibody.";				
RT	J. Cell Sci. 114:539-547(2001).				
RL	[4]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RC	TISSUE=Brain;				
RX	MEBLINB=21154917; PubMed=11230166; DOI=10.1101/gr.154701;				
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber U., Glaesl S.,				
RA	Amorje W., Boecher M., Bloeker H., Baerzachs S., Blum H.,				
RA	Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,				
RA	Mewes H.-W., Olterswalder B., Obermaier B., Tampe J., Heubner D.,				
RA	Wandert R., Korn B., Klein M., Poustka A.;				
RT	"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";				
RT	Genome Res. 11:422-435(2001).				
RL	[5]				
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RP	MEBLINB=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;				
RX	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,				
RA	Chen J., Chow B., Chu C., Crowley C., Currell B., Duell B., Dowd P.,				
RA	Bacon D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,				

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sehabiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandend R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
 RA Yansua D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.,
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.",
 RL Genome Res. 13:2265-2270(2003).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RC TISSUE=Ovary;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Udell T.B., Toshimuki S., Carminci P., Prange C.,
 RA Raha S.S., Loquiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson K.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schrein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP PROTEIN SEQUENCE OF 28-103 AND 123-130, AND N-GLYCOSYLATION.
 RX PubMed=7646439;
 RA Naik U.P., Ehrlich Y.H., Kornecki E.,
 RT "Mechanisms of platelet activation by a stimulatory antibody: cross-
 RT linking of a novel platelet receptor for monoclonal antibody FII with
 RT the Fc gamma RII receptor.",
 RL Biochem. J. 310:155-162(1995).
 RN [8]
 RP PROTEIN SEQUENCE OF 28-42.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Hensel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.",
 RL Protein Sci. 13:2819-2824(2004).
 RN [9]
 RP PROTEIN SEQUENCE OF 28-39.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goehals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.,
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.",
 RL Nat. Biotechnol. 21:566-569(2003).
 RN [10]
 RP INTERACTION WITH MPDZ.
 RX PubMed=11489913; DOI=10.1083/jcb.200103047;
 RA Itoh M., Sasaki H., Furuse M., Ozaki H., Kita T., Tsuchida S.,
 RT "Functional adhesion molecule (UAM) binds to PAR-3: a possible
 RT mechanism for the recruitment of PAR-3 to tight junctions.",
 RL J. Cell Biol. 154:491-497(2001).
 RN [11]
 RP REVIEW, AND NOMENCLATURE.
 RX PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
 RA Muller W.A.,
 RT "Leukocyte-endothelial cell interactions in leukocyte transmigration
 RT and the inflammatory response.",
 RL Trends Immunol. 24:327-334(2003).
 CC -1- FUNCTION: Seems to plays a role in epithelial tight junction

CC formation. Appears early in primordial forms of cell junctions and
 CC recruits PAR3. The association of PAR3 with JAM1, thereby preventing
 CC prevent the interaction assembly (By similarity). Plays a role in
 CC tight junction assembly (By similarity). Plays a role in
 CC regulating monocyte transmigration involved in integrity of
 CC epithelial barrier. Involved in platelet activation.
 CC -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 CC association between PAR3 and PAR6B probably disrupts this
 CC interaction (By similarity). Interacts with the ninth PDZ domain
 CC of MPDZ.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC localized at tight junctions of both epithelial and endothelial
 CC cells.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
 CC domains.
 CC -----
 CC EMBL: AF111713; AAD42050.1; -; mRNA.
 CC EMBL: AF207907; AAF22829.1; -; mRNA.
 CC EMBL: AF172398; AAD48877.1; -; mRNA.
 CC EMBL: AL136649; CAB66584.1; -; mRNA.
 CC EMBL: AY358896; AAQ89255.1; -; mRNA.
 CC EMBL: BC001533; AAH01533.1; -; mRNA.
 CC PIR: A59406; S56749.
 CC PDB: 1NBO; X-ray; A/B=27-233.
 CC EMBL: ENSG00000158769; Homo sapiens.
 CC HGN: HGNC:14685; F11R.
 CC MIM: 605721; -;
 CC GO: GO:0005911; C:intercellular junction; TAS.
 CC GO: GO:0006954; P:inflammatory response; TAS.
 CC InterPro: IPR007110; Ig-like.
 CC DR Pfam: PF00047; Ig_1.
 CC DR PROSITE: PS50835; IG_LIKE_2.
 CC 3D-structure: Direct protein sequencing; Glycoprotein;
 CC Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
 CC FT CHAIN 1 27
 CC FT SIGNAL 1 27
 CC FT TOPO_DOM 28 238
 CC FT TRANSMEM 239 259
 CC FT TOPO_DOM 260 299
 CC FT DOMAIN 28 125
 CC FT DOMAIN 135 228
 CC FT CARBOHYD 185 185
 CC FT DISULFID 50 109
 CC FT DISULFID 153 212
 CC SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;
 CC Query Match 100.0%; Score 1544; DB 1; Length 299;
 CC Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 CC Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MGTQAQYERKLTCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVLTSCAYSGFSSPRV 60
 CC DB 1 MGTQAQYERKLTCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVLTSCAYSGFSSPRV 60
 CC QY 61 EKWFDQDDTRLVLCYNNKIRASVEDRTPFPTGITPKSVREDTGYTCVNSSEGGNSYG 120
 CC DB 61 EKWFDQDDTRLVLCYNNKIRASVEDRTPFPTGITPKSVREDTGYTCVNSSEGGNSYG 120
 CC QY 121 EVKVKLIVLPSPKPTVNISSATIGNRAVLTCSEBODSPSESEYTFPKDGIWNPMPKST 180
 CC DB 121 EVKVKLIVLPSPKPTVNISSATIGNRAVLTCSEBODSPSESEYTFPKDGIWNPMPKST 180
 CC QY 121 EVKVKLIVLPSPKPTVNISSATIGNRAVLTCSEBODSPSESEYTFPKDGIWNPMPKST 180
 CC DB 121 EVKVKLIVLPSPKPTVNISSATIGNRAVLTCSEBODSPSESEYTFPKDGIWNPMPKST 180
 CC QY 181 RAFSNSSYVNLPTTGGELVFPDPLASDPTGEYSCEARNGYGTPTMTSNARMAVERNVGIV 240
 CC DB 181 RAFSNSSYVNLPTTGGELVFPDPLASDPTGEYSCEARNGYGTPTMTSNARMAVERNVGIV 240

QY 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSASEGFKQTSSFLV 299
 DB 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSASEGFKQTSSFLV 299

RESULT 2
 06FIB4_HUMAN
 ID 06FIB4_HUMAN PRELIMINARY; PRT; 299 AA.
 AC 06FIB4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE F11R protein (F11 receptor protein) (JMW1) (Hypotheetical protein
 DE F11R0671). ORFNames=RP11-544M22.2-001;
 GN Name=F11R; ORFNames=RP11-544M22.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20537955; PubMed=11087121; DOI=10.1080/15216540050176593;
 RA Gupta S.K., Pillaiarsetti K., Ohlstein E.H.;
 RT "platelet agonist F11 receptor is a member of the immunoglobulin
 RT superfamily and identical with junctional adhesion molecule (JAM);
 RT regulation of expression in human endothelial cells and macrophages.";
 RL JMBB Life 50:51-56(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22701983; PubMed=12817473; DOI=10.1515/BC.2003.085;
 RA Wenzel K., Felix S.B., Flachmeier C., Heere P., Schulze W.,
 RA Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.,
 RA Hoehne M.R.;
 RT "Identification and characterization of KAT, a novel gene
 RT preferentially expressed in several human cancer cell lines.";
 RL Biol. Chem. 384:763-775(2003).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RA Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J.,
 RA Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,
 RA Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,
 RA Aotaka S., Sasaki N., Hattori A., Okumura K., Negai K., Sugano S.,
 RA Isogai T.;
 RT "Signal Sequence and Keyword Trap in silico for Selection of Full-
 RT length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
 RT capped cDNA libraries.";
 RL DNA Res. 12:117-126(2005).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Kainine N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Pheasant M., Farmer A.;
 RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
 RT vector.";
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Harrison E.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CFS33312; CAG38543.1; -; mRNA.
 DR EMBL: AF191495; AAC8379.1; -; mRNA.
 DR EMBL: AF490407; AAC84556.1; -; Genomic DNA.
 DR EMBL: BT020103; AAV38906.1; -; mRNA.
 DR EMBL: AL518106; CA115365.1; -; Genomic DNA.
 DR EMBL: AK075152; BAC11436.1; -; mRNA.
 DR SMR; 06FIB4; 25-233.

DR Ensembl; ENSG00000158769; Homo sapiens.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KM Receptor.
 SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 100.0%; Score 1544; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 1,8e-111;
 Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTRAOYERKLLCLFLAATLCSLALGSYTVHSSSEPVRIPENNPVKLSGAYSGFSSPRV 60
 DB 1 MGTRAOYERKLLCLFLAATLCSLALGSYTVHSSSEPVRIPENNPVKLSGAYSGFSSPRV 60

QY 61 EMKFDGDTTRLVCYNNKLTASVEDRVTPLPTGITFKSVTREDTGYTCWVSEGGNSYG 120
 DB 61 EMKFDGDTTRLVCYNNKLTASVEDRVTPLPTGITFKSVTREDTGYTCWVSEGGNSYG 120

QY 121 EVRYKLIIVPSPKPTVNISSATTIGNRAVLTCSEDDGSPSEYTFKQGIWPTNPKST 180
 DB 121 EVRYKLIIVPSPKPTVNISSATTIGNRAVLTCSEDDGSPSEYTFKQGIWPTNPKST 180

QY 181 RAPSNSYVLPNTTGLVPLPSADPTGEYSCEARNGYGRPMNSNVRMAYERNVIV 240
 DB 181 RAPSNSYVLPNTTGLVPLPSADPTGEYSCEARNGYGRPMNSNVRMAYERNVIV 240

QY 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSASEGFKQTSSFLV 299
 DB 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSASEGFKQTSSFLV 299

RESULT 3
 09Y5B2_HUMAN
 ID 09Y5B2_HUMAN PRELIMINARY; PRT; 259 AA.
 AC 09Y5B2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Junction adhesion molecule.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reeves T.A., Pochet M.,
 RA Foley C., Parkos C.A.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL: AF154005; AAD43794.1; -; mRNA.
 DR HSP: O9Y624; INBO.
 DR SMR; 09Y5B2; 20-193.
 DR Ensembl; ENSG00000158769; Homo sapiens.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin domain; Transmembrane.
 SQ SEQUENCE 259 AA; 28122 MW; FE38521A911582D0 CRC64;

Query Match 83.0%; Score 1281; DB 2; Length 259;
 Best Local Similarity 86.0%; Pred. No. 3,8e-91;
 Matches 257; Conservative 0; Mismatches 2; Indels 40; Gaps 2;

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QY 1 MGTRKQVERKLLCLFLIATILLCSLALGSVTHSSPEPERIPENNPKVLCSCAYSGFSSPRV 60
DB 1 MGTRKQVERKLLCLFLIATILLCSLALGSVTHSSPEPERIPENNPKVLCSCAYSGFSSPR- 39
QY 61 EWMKFDQDTRRLVCYNNKIRASVEDRYTFLPTGITFKSVTRREDTGYTCWVSEBGSNSYG 120
DB 40 -----AASYEDRYTFLPTGITFKSVTRREDTGYTCWVSEBGSNSYG 80
QY 121 EVKVKLIVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 180
DB 81 EVKVKLIVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 140
QY 181 RAFSNSSVYNPTTGGELVFPDPLASDGTGEYSCEARNYCGFPMTSNAYRMAVERNVGIV 240
DB 141 RAFSNSSVYNPTTGGELVFPDPLASDGTGEYSCEARNYCGFPMTSNAYRMAVERNVGIV 200
QY 241 AAVLVTLILGLIVFGIWFAYSRGHPDRTKKGTSKKVIYSPSARSEGEFKQTSFLV 299
DB 201 AAVLVTLILGLIVFGIWFAYSRGHPDRTKKGTSKKVIYSPSARSEGEFKQTSFLV 259

RESULT 4
JAM1_BOVIN STANDARD; PRT; 298 AA.
AC 09XT56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion molecule 1) (JAM).
GN Name=JAM1; Synonyms=JAM1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=99323940; PubMed=10395639;
RA Ozaki H., Ishii K., Horikuchi H., Arai H., Kawamoto T., Okawa K., Iwamatsu A., Kita T.;
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557(1999).
CC -1- FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PAR3. The association of the PAR3-PAR3 complex may prevent the interaction of PAR3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.
CC -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The association between PAR3 and PAR3B probably disrupts this interaction. Interacts with the ninth PDZ domain of MPDZ (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Localized at tight junctions of both epithelial and endothelial cells (By similarity).
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like) domains.
CC -----
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CC -----
CC EMBL; AF111714; AAD42051.1; -; mRNA.
DR HSSP; Q9Y624; INBO.
DR SMR; Q9XT56; 24-232.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; Igc2_1.
DR PROSITE; PSS0835; IG_LIKE_2.
KW Glycoprotein; Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 298 Junctional adhesion molecule A.
FT TOPO_DOM 25 237 Extracellular (Potential).
FT TRANSMEM 238 258 Potential.
FT TOPO_DOM 259 298 Cytoplasmic (Potential).
FT DOMAIN 28 124 Ig-like V-type 1.
FT DOMAIN 134 227 Ig-like V-type 2.
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT DISULFID 49 108 Potential.
FT DISULFID 152 211 Potential.
SQ SEQUENCE 298 AA; 32456 MW; 714FE1C1714769A2 CRC64;

Query Match 76.2%; Score 1176.5; DB 1; Length 298;
Best Local Similarity 74.6%; Pred. No. 5,6e-83;
Matches 223; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 1 MGTRKQVERKLLCLFLIATILLCSLALGSVTHSSPEPERIPENNPKVLCSCAYSGFSSPRV 60
DB 1 MGTRKAKGSTLELLF-TSMILCSIALGRGAVQTEPVVRVBNPPALCSYSGFSSPRV 59
QY 61 EWMKFDQDTRRLVCYNNKIRASVEDRYTFLPTGITFKSVTRREDTGYTCWVSEBGSNSYG 120
DB 60 EWMKFDHIDGLVCYNNKIRASVENRYTFSDDTGIITHSVTRKDTGATCWVSEBGNITYG 119
QY 121 EVKVKLIVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 180
DB 120 EVYVQGLIVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTWFKDGIWPTNPKST 179
QY 181 RAFSNSSVYNPTTGGELVFPDPLASDGTGEYSCEARNYCGFPMTSNAYRMAVERNVGIV 240
DB 180 RAFSNSSVYNPTTGGELVFPDPLASDGTGEYSCEARNYCGFPMTSNAYRMAVERNVGIV 239
QY 241 AAVLVTLILGLIVFGIWFAYSRGHPDRTKKGTSKKVIYSPSARSEGEFKQTSFLV 299
DB 240 AAVLVTLILGLIVFGIWFAYSRGHPDRTKKGTSKKVIYSPSARSEGEFKQTSFLV 298

RESULT 5
QSE9V8_BOVIN PRELIMINARY; PRT; 298 AA.
AC QSE9V8;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE F11 receptor isoform a.
GN Name=F11r;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grose W.M., Preking B.A., Roberts A.J., Stone R.T., Csaas E., Wray J.E., White J., Cho J., Fahrreng S.C., Bennett G.L., Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Mckown C.G., Perteza G., Holt I., Karaymicheva S., Liang F., Queckenbush J., Keeler J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine CDNA RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled;
RA Hatnay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keeler J.W.,

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RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 RT clones."
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT020812; AAX08829.1; -, mRNA.
 KM Receptor.
 SO SEQUENCE 298 AA; 32456 MW; 714F61C1714769A2 CRC64;

Query Match 76.2%; Score 1176.5; DB 2; Length 298;
 Best Local Similarity 74.6%; Pred. No. 5.6e-83;
 Matches 223; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 1 MGTAQVERKLCFLAAILCSIALGVTWHSSEPEVRIPENNPKLSCAYSGFSSPRV 60
 DB 1 MGTAKVGSTELLP-TSMILGSLALGCAVQTEBPVAVPENNAKLSCSYSGFSSPRV 59
 QY 61 EMKFDGDTTRLVCCYNKKTASYEDRYVFLPTGTFKSVTRBEDGTTCWVSEGGNSYG 120
 DB 60 EMKFTGDIRGLVCYNKKTASYENRYVFSPTGITFHSVTRKDTCTWTCWSDGGNTYG 119
 QY 121 EVKVKLVLPSPKPTVNPSSATIGNRAVLTCSEODGSPSEXTWFKDGIWMPNPKST 180
 DB 120 EVTVQLIVLPSPKPTVNPSSVITGTRAVLTCSEBDGSPSEYKWFQGVEMPLEPKSN 179
 QY 181 RAFNSSSVYLNPTTGLVFPDPLASDTGEYSCEARNGVTGMTSNVAVMEAVENRYIV 240
 DB 180 RAFNSSTYLNQKGLVFPDPLASDTGDTQAOONGYASVPKSDTVAMDVELNVGIV 239
 QY 241 AAVLVTLILGLILVFGIWFAYSRGHPDRTRKKGTSKKVIYQPSARSGEFGKQTSSFLV 299
 DB 240 AAVVTLILGLALFGIWFAYSRCYFDPKAKKGTSNKVIYQPSARSGEFGKQTSSFLV 298

RESULT 6
 JAM1 RAT STANDARD; PRT; 300 AA.
 AC O9JHY1;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DE Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion molecule 1) (JAM).
 GN Name:Fltr; Synonyms=Jam1;
 OS Rattus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (MRNA).
 RC STRAIN=Sprague-Dawley;
 RA Mashima H., Kojima I.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RC TISSUE=Prostate;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Seems to play a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PAR3. The association of the PAR6-PAR3 complex may prevent the interaction of PAR3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier.
 CC Involved in platelet activation (By similarity).
 CC -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The association between PAR3 and PAR6B probably disrupts this interaction. Interacts with the ninth PDZ domain of MPDZ (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC Localized at tight junctions of both epithelial and endothelial cells (By similarity).
 CC -1- PTM: N-Glycosylated (By similarity).

CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like) domains.
 CC -----
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 CC -----
 CC EMBL; AF276998; AAF78250.1; -, mRNA.
 CC EMBL; BC065309; AA65309.1; -, mRNA.
 CC HSSP; O88792; 1P97.
 CC SMR; O9JHY1; 27-238
 CC Ensembl; ENSRNOG0000004414; Rattus norvegicus.
 CC RGD; 621842; Fltr.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_v.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; Igv; 1.
 CC PROSITE; PS50835; Ig_Like; 2.
 CC Glycoprotein; Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
 CC SIGNAL 1 26 Potential.
 CC CHAIN 27 300 Junctional adhesion molecule A.
 CC TOPO_DOM 27 238 Extracellular (Potential).
 CC TRANSMEM 239 259 Potential.
 CC TOPO_DOM 260 300 Cytoplasmic (Potential).
 CC DOMAIN 28 122 Ig-like V-type 1.
 CC DOMAIN 134 228 Ig-like V-type 2.
 CC CARBOHYD 185 185 N-linked (GlcNAc..) (Potential).
 CC FT DISULFID 49 106 By similarity.
 CC FT DISULFID 152 212 By similarity.
 CC SQ SEQUENCE 300 AA; 32370 MW; 45AE362A96158BFA CRC64;

Query Match 71.0%; Score 1096.5; DB 1; Length 300;
 Best Local Similarity 71.8%; Pred. No. 9e-77;
 Matches 216; Conservative 33; Mismatches 49; Indels 3; Gaps 3;

QY 1 MGTAQVERKLCFLAAILCSIALGVTWHSSEPEVRIPENNPKLSCAYSGFSSPRV 60
 DB 1 MGTGKAGSKLFLF-TSMILGSLVQKGSYSPQTAIVQPDNSVTLPCISGFSSPRV 59
 QY 61 EMKFDGDTTRLVCCYNKKTASYEDRYVFLPTGTFKSVTRBEDGTTCWVSEGGNSYG 120
 DB 60 EMKFGQSTALVCYNKQITVYPADRYTFSSSGITFSSVTRKDNGETCWVSEGGQNYG 119
 QY 121 EVKVKLVLPSPKPTVNPSSATIGNRAVLTCSEODGSPSEXTWFKDGIWMPNPKS 179
 DB 120 EVSIHLTVLPSPKPTVNPSSVITIGNRAVLTCSEHDSGSPSEYSWFKDGVPMILADAKK 179
 QY 180 TRAFNSSSVYLNPTTGLVFPDPLASDTGEYSCEARNGVTGMTSNVAVMEAVENRYIV 239
 DB 180 TRAFINSSTYIIDPSGDLVFPDPLASDTGEYSCEARNGVTGTAARSEAVRMEAVLNVGCI 239
 QY 240 VAAVLVTLILGLILVFGIWFAYSRGHPDRTRKKGTS-SKKVIYQPSARSGEFGKQTSSFL 298
 DB 240 VAAVLVTLILGLILFGIWFAYSRCYFERTKKGTAPEKVIYQPSARSGEFGKQTSSFL 299
 QY 299 V 299
 DB 300 V 300

RESULT 7
 O8VC3 MOUSE PRELIMINARY; PRT; 300 AA.
 ID O8VC3;
 AC O8VC3;
 DT 01-MAR-2002 (TRENBERG, 20, Created)
 DT 01-MAR-2002 (TRENBERG, 20, Last sequence update)
 DT 13-SEP-2005 (TRENBERG, 31, Last annotation update)
 DE Fltr protein (Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130004G24 product:junction cell adhesion


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Db      1  MGTGKAKRKLPLF-TSMIGSLVQKGSVYTAQSDVQVENESEIKLCTYSGSSPRV 59
Qy      61  EWKFDGDTRLVLCVNNKITASyEDRVTLFPTGITFKSVTRDGTYYTQWSEEGNSYG 120
Db      60  EWKFQGSTALVVCNNSGITAPYADRVTFSSSGITFFSVTRKNDNEYTCWVSEEGQNYG 119
Qy      121  EVKRYKLVLVPPSKPTVNIPISSATIGNAVLTCSSQDSSPSEYTWFDQGVMP1-NPKS 179
Db      120  EVSHLTLVLPSPSKPTISVPSVITGNRAVLTCSEHDSPPSEYSWFDGISM1LADAKK 179
Qy      180  TRAFNSNSYVNPPTGELVFPDPLASDPGEYSCEARNGYGTPTMTSNAVMEAVERNVGI 239
Db      180  TRAFNNSFTIDPKSGDLIFDPVTA,FDSGEYTCQAKNGYGRAMSEAAHMAVELNVGCI 239
Qy      240  VAAVLVTLILGLIFGVIMFAYSRGHPDRITKGTG-SKRVITYQPSARSEGEFKQTSFL 298
Db      240  VAAVLVTLILGLIFGVIMFAYSRGHPDRITKGTG-SKRVITYQPSARSEGEFKQTSFL 299
Qy      299  V 299
Db      300  V 300

RESULT 8
JAM1_MOUSE STANDARD; PRT; 300 AA.
AC 086792;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion
DE molecule 1) (JAM).
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98327120; PubMed=9660867; DOI=10.1083/jcb.142.1.117;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Finocchia P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana B.;
RT "Junctional adhesion molecule, a novel member of the immunoglobulin
RT superfamily that distributes at intercellular junctions and modulates
RT monocyte transmigration.";
RL J. Cell Biol. 142:117-127(1998).
[2]
RN SUBCELLULAR LOCATION.
RP MEDLINE=20489356; PubMed=11036763;
RA Aurrand-Lione M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an emerging junctional adhesion molecular
RT family?";
RL EMBO J. 20:3738-3748(2001).
[3]
RN INTERACTION WITH PARD3.
RP MEDLINE=21340266; PubMed=11447115; DOI=10.1093/emboj/20.14.3738;
RA Ebner K., Suzuki A., Horikoshi Y., Hirose T.,
RA Meyer zu Bruckwede M.-K., Ohno S., Vestweber D.;
RT "The cell polarity protein ASIP/PAR-3 directly associates with
RT junctional adhesion molecule (JAM).";
RL EMBO J. 20:3738-3748(2001).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RP MEDLINE=21391702; PubMed=11500366; DOI=10.1093/emboj/20.16.4391;
RA Koestrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA Schmid G., Mueller P., Bazzoni G., Dejana B., Bartfal T.,
RA Winkler F.K., Henning M.;
RT "X-ray structure of junctional adhesion molecule: structural basis for
RT homophilic adhesion via a novel dimerization motif.";
RL EMBO J. 20:4391-4398(2001).

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RN      (5)
RP REVIEW, AND NOMENCLATURE.
RX MEDLINE=22695901; PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA Muller W.A.;
RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT and the inflammatory response.";
RL Trends Immunol. 24:327-334(2003).
CC -1- FUNCTION: Seems to play a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PARD3. The association of the PARD6-PARD3 complex may
CC prevent the interaction of PARD3 with JAM1, thereby preventing
CC tight junction assembly. Plays a role in regulating monocyte
CC transmigration involved in integrity of epithelial barrier.
CC Involved in platelet activation.
CC -1- SUBUNIT: Interacts with the ninth PDZ domain of MPDZ (By
CC similarity). Interacts with the first PDZ domain of PARD3. The
CC association between PARD3 and PARD6 probably disrupts this
CC interaction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC localized at tight junctions of both epithelial and endothelial
CC cells.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U89915; AAC32982.1; -; mRNA.
DR PDB; 1P97; X-ray; A=27-238.
DR Ensembl; ENSMUSG00000038235; Mus musculus.
DR MGI; MGI:1321398; F11r.
DR GO; GO:0005923; C:tight junction; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0030855; P:epithelial cell differentiation; IDA.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; Ig_Like; 2.
KW 3D-structure; Glycoprotein; Immunoglobulin domain; Repeat; Signal;
KW Tight junction; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 300
FT TOPO_DOM 27 238
FT TRANSMEM 239 259
FT TOPO_DOM 260 299
FT DOMAIN 28 122
FT DOMAIN 134 230
FT CARBOHYD 42 42
FT CARBOHYD 185 185
FT DISULFID 49 108
FT DISULFID 152 212
FT STRAND 29 31
FT STRAND 36 40
FT TURN 41 42
FT STRAND 45 48
FT STRAND 50 52
FT STRAND 57 67
FT TURN 66 67
FT STRAND 68 74
FT TURN 75 76
FT STRAND 77 78
FT HELIX 80 82
FT TURN 83 85
FT STRAND 86 89
FT TURN 90 91
FT STRAND 92 95
FT HELIX 100 102

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FT STRAND 104 112
 FT TURN 113 114
 FT STRAND 118 129
 FT STRAND 135 137
 FT STRAND 141 143
 FT TURN 144 145
 FT STRAND 148 153
 FT STRAND 158 158
 FT STRAND 162 167
 FT TURN 168 169
 FT STRAND 170 171
 FT STRAND 173 173
 FT STRAND 181 181
 FT STRAND 188 190
 FT TURN 192 194
 FT STRAND 197 199
 FT HELIX 204 206
 FT STRAND 208 215
 FT STRAND 222 223
 FT STRAND 227 232
 SQ SEQUENCE 300 AA; 32369 MW; 391F3E48FF3B97EC CRC64;

Query Match 69.5%; Score 1073.5; DB 1; Length 300;
 Best Local Similarity 68.1%; Pred. No. 5.5e-75;
 Matches 205; Conservative 44; Mismatches 49; Indels 3; Gaps 3;

QY 1 MGTAAQVBRKLLCFILAILCSLALGSVTVHSSSEPEVRIENNPVKLSCAVSGFSSPRV 60
 DB 1 MGTGKAGKRLFLF-TSMILGSLVQKGSVYTAQSDVQVBNESIKLCTYSGFSSPRV 59
 QY 61 EMKEDQDTRRLVCYNNKITASYEDRYVFLPTGTFKSVTEPDGYTCWVSEGGNSYG 120
 DB 60 EMKVGQSTRLVCYNSGITAPYADRYTFSSSGITFFSVTRKDGTYTCWVSEGGNYG 119
 QY 121 EVVKYKLVLPSPKPTVNISSATIGNRAVLTCSEODSPSEXYTWPKDGIWPT-NPKS 179
 DB 120 EVSHLTVLPSPKPTISVPSVITIGNRAVLTCSEHODSPSEXYTWPKDGIWPTADAKK 179
 QY 180 TRAFNSNSVYLPPTTGGELVFPPLASDTGEYSCENRNGYGTPTMSNAVRMVAVERANGVI 239
 DB 180 TRAFNNSFTIDPFGSLIDFPVTAFPDSEGYCOAONGYGTAMKSEAHMDAVELNAGGI 239
 QY 240 VAAVLVTLILGLVFGIWFPAYSRGGHFDRTKKGTS-SKVVYISQPSARSSEGEFKOTSSFL 298
 DB 240 VAAVLVTLILGLIFGWPAYSRGGYFETTKKGTAIPGKAVIYQPSSTRSEGEFKOTSSFL 299
 QY 299 V 299
 DB 300 V 300

RESULT 9
 ID Q9JUD5_RAT PRELIMINARY; PRT; 173 AA.
 AC Q9JUD5;
 DT 01-OCT-2000 (Tremblrel. 15. Last Created)
 DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
 DE Junctional adhesion molecule (Fragment).
 GN Name=Fli1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kirsch T., Wellner M., Haller H., Lippold A.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF241261; AAFe1729.1; -; mRNA.
 DR HSSP; O86792; 1F97.
 DR SMR; Q9JUD5; 1-111.
 DR RGD; 621842; Fli1.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00408; IgC2; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON TER 1
 SQ SEQUENCE 173 AA; 18706 MW; 3EE3ECDF5AFB8B2 CRC64;

Query Match 45.3%; Score 700; DB 2; Length 173;
 Best Local Similarity 79.8%; Pred. No. 2.5e-46;
 Matches 138; Conservative 16; Mismatches 17; Indels 2; Gaps 2;

QY 129 LVPSKPTVNISSATIGNRAVLTCSEODSPSEXYTWPKDGIWPT-NPKSTRAFSSNS 187
 DB 1 LVPSKPTVNISSATIGNRAVLTCSEHODSPSEXYTWPKDGIWPTADAKKTRAFINSS 60
 QY 188 VYLNPTTGGELVFPPLASDTGEYSCENRNGYGTPTMSNAVRMVAVERANGVIYAAVLVTL 247
 DB 61 YTIIDPKSGDLVPDVSAPFDSGEYCEAONGYGTAMKSEAVRMVAVELNAGIYAAVLVTL 120
 QY 248 ILGLVFGIWFPAYSRGGHFDRTKKGTS-SKVVYISQPSARSSEGEFKOTSSFLV 299
 DB 121 ILGLIFGIWFPAYSRGGYFETTKKGTAIPGKAVIYQPSARSSEGEFKOTSSFLV 173

RESULT 10
 ID Q7ZWTO_XENLA PRELIMINARY; PRT; 289 AA.
 AC Q7ZWTO;
 DT 01-JUN-2003 (Tremblrel. 24. Created)
 DT 01-JUN-2003 (Tremblrel. 24. Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26. Last annotation update)
 DE MG53721 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tothiyukl S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muljaby S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Vallalath D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.


```
RESULT 14
06J15_XENTR PRELIMINARY; PRT; 291 AA.
ID 06J15_XENTR PRELIMINARY; PRT; 291 AA.
AC 06J15_XENTR PRELIMINARY; PRT; 291 AA.
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE MGC79514 protein.
GN Name=MGC79514;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
CX NCBI_TaxID=8364;
RN NM_111
NC NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Cantin P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S., Schein J.E., Jones S.J.M., Skalski U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN NM_121
NC NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhardt D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC080901, AA80901.1; -, mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_2.
DR SMART: SM00408; IG2_2.
DR PROSITE: PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 291 AA; 31538 MW; D6A3115178E222A6 CRC64;
```

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Query Match 36.3%; Score 560.5; DB 2; Length 291;
Best Local Similarity 40.9%; Pred. No. 3.1e-35;
Matches 123; Conservative 54; Mismatches 105; Indels 19; Gaps 9;
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```
QY 5 AQRKRLCLFLILILCSLALGVTYVSSSEPEVRIPENNPVKLSGAYSGSSPRVEMK 63
DB 4 ASSNRGAVVGLCLCLCTAAAPAGVS--TPNPTTVKCGATRADLCITTSDDTSKRVEMK 61
QY 64 FDGD-D-TRRLVCYNNKITASYEDRVTFPLPTGTFKSVTRDPTGYTCMVSEEGNS--Y 119
DB 62 FVNQQLERFFVYDDDTLFTASVYNNRATSVPOGIIINQITISKDAGEVSCVETSVDSNGOTLY 121
QY 120 GEVVKVILVLPSPKPTVNISSATIGRAVAVTCSEQDGSPPSEETVFKDGIWMPNPKS 179
DB 122 GEAATQILVIVAPSPQPMHAPVAVTATGAVELRCVETGYPPTPTVYONKAPMPPNQO- 180
QY 180 TRASNSSYVNPPTTGGELVFPDPLASDPTGEYSCEARNGVGTMTSNAAVMEAVENGVY 239
DB 181 -----NATYITDPTGTVLKFRAVAVASDSGDYTCRAANSEG--EQVSATVIRMVAVQDVGCI 234
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QY 240 VAAVLYTLILGLVFGIWPAYSRGHPRTRKGTSSKKVIYSQPS-ARSEGEFKOTSSFL 298
DB 235 VAAVLYTLILGLVFGIWPAYSRGYLD--KKG--NRKVYSQPSRSTDKNFOQTSSFL 290
QY 299 V 299
DB 291 V 291
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RESULT 15
Q4S828_TETNG PRELIMINARY; PRT; 260 AA.
ID Q4S828_TETNG PRELIMINARY; PRT; 260 AA.
AC Q4S828_TETNG PRELIMINARY; PRT; 260 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 7 SCAP14703, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00022119001.
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
CX NCBI_TaxID=99883;
RN NM_111
NC NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dosset C., Segreus B.,
RA Daetliwa C., Salanoubat M., Levy M., Boulet N., Castelano S.,
RA Anthonard V., Jabin C., Castel V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Catroilo L., Poulain J., De Bernardinis V.,
RA Crnaud C., Duprat S., Brotier P., Coutanceau J.P., Gauzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croillius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957 (2004).
RN NM_121
NC NUCLEOTIDE SEQUENCE.
RC Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, CA601014703; CAG02884.1; -, Genomic DNA.
FT NON TER 260
SQ SEQUENCE 260 AA; 28017 MW; 7D8EA67FCA13CAAF7 CRC64;
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Query Match 34.6%; Score 534.5; DB 2; Length 260;
Best Local Similarity 42.6%; Pred. No. 2.8e-33;
Matches 110; Conservative 42; Mismatches 99; Indels 7; Gaps 4;
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QY 12 LCLFLILILCSLALGVTYVSSSEPEVRIPENNPVKLSGAYSGSSPRVEMKPD--QG 67
DB 5 VAAVMAAFLLSATGCGSVTTKSEVGENNGDLCTYSADRGPARVEMKFNKILQG 64
QY 68 DTRRLVCYNNKITASYEDRVTFPLPTGTFKSVTRDPTGYTCMVSEEGNSYGEVVKLI 127
DB 65 SQVYVV-FDGAFTPEYPSRLTMVNSLRFSAVTRKXNGVDFCEVS--GNGQFOEVRVLT 121
QY 128 VLPSPKPTVNISSATIGRAVAVTCSEQDGSPPSEETVFKDGIWMPNPKSSTRAFSSSS 187
DB 122 VLPSPSPVPCNIPSSVTTGGATATDCNDPDDSPPTVRYRNKGVLPADPESKISGYQVAT 181
QY 188 VYLPNPTTGGELVFPDPLASDPTGEYSCEARNGVGTMTSNAAVMEAVENGVYVAAVLYTL 247
DB 182 YSLDEIGLKLITYSKTSSDSGEYTCFAVNVKAGPQRCRAVMEVRDLMTGGIVAGVIAL 241
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Qy	248	ILGLIVEGIWFAYSRGH	265
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Db	242	LILALIVEGIWYANKGY	259

Search completed: May 16, 2006, 07:07:42
Job time : 271 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 07:01:24 ; Search time 40 Seconds
(without alignments)
719.220 Million cell updates/sec

Title: US-10-785-433-1
Perfect score: 1544
Sequence: 1 MGTAKQVERKLLCLFILAIL.....YSPSANSBGEFKOTSSFLV 299

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1544	100.0	299	2 S56749	junctional adhesio
2	196	12.7	365	2 JC7780	coxsackie- and ade
3	189.5	12.3	7962	2 J38346	elastic titin - hu
4	181.5	11.8	862	2 A49583	differentiation an
5	181.5	11.8	868	2 A46512	CD22 homolog/B lym
6	179	11.6	538	2 JC2457	vascular cell adhe
7	178.5	11.6	847	2 JH0371	B-cell adhesion pr
8	178	11.5	483	2 T17346	hypothetical prote
9	177.5	11.5	647	2 A35648	B-cell adhesion pr
10	177.5	11.5	1273	2 T32405	saar-3 protein - Ca
11	172.5	11.2	1227	2 T33004	hypothetical prote
12	171	11.1	1091	2 A58532	glial cell membran
13	169.5	11.0	765	2 C42632	cell adhesion mole
14	169.5	11.0	812	2 B42632	cell adhesion mole
15	169.5	11.0	932	2 A42632	cell adhesion mole
16	169.5	11.0	2222	2 T13924	sdh protein - frui
17	169	10.9	739	2 JN0581	vascular cell adhe
18	167.5	10.8	423	2 T29549	hypothetical prote
19	167.5	10.8	1896	2 T08851	Down syndrome cell
20	166	10.8	584	2 T08678	hypothetical prote
21	166	10.8	5175	2 T20992	hypothetical prote
22	166	10.8	5198	2 T43290	hemiscentin precurs
23	165.5	10.7	4162	2 T42633	connectin/citin -
24	165	10.7	344	2 A27681	non-specific cross-
25	165	10.7	6642	2 T29757	protein UNC-89 - C
26	163.5	10.6	875	2 T33434	hypothetical prote
27	160	10.4	1051	2 A39712	kinase-like protei
28	160	10.4	1328	2 T23007	hypothetical prote
29	158	10.2	1040	2 A49356	transient axonal g

30	158	10.2	1091	1 JTCNLT	neural cell adhesi
31	157.5	10.2	725	2 JEO099	neural cell adhesi
32	157.5	10.2	1088	1 JUXNLT	neural cell adhesi
33	157.5	10.2	1323	2 FN0568	connectin 38 - chi
34	157	10.2	1199	2 T23005	hypothetical prote
35	156	10.1	1015	2 T32186	hypothetical prote
36	156	10.1	1040	2 A34695	axonal glycoprotei
37	155.5	10.1	521	2 A34338	biliary glycoprote
38	155.5	10.1	799	2 S18209	fibroblast growth
39	155.5	10.1	858	1 JLRINC	neural cell adhesi
40	155.5	10.1	1499	2 J50212	protein-tyrosine-p
41	155	10.0	1070	2 JC4593	protein-tyrosine k
42	154	10.0	739	2 J50675	vascular cell adhe
43	154	10.0	761	1 JLRUNG	neural cell adhesi
44	154	10.0	1256	2 T03096	CD0 protein - rat
45	153.5	9.9	853	1 J0BONC	neural cell adhesi
46	153	9.9	344	2 I56551	neuroglimin - rat
47	153	9.9	1239	1 A32579	neuroglian - fruit
48	153	9.9	1260	1 S05479	neural cell adhesi
49	153	9.9	1338	2 S09982	protein-tyrosine k
50	152	9.8	338	2 UC4776	limbic-system-asso
51	152	9.8	1036	2 S22383	axonin I precursor
52	152	9.8	1257	1 A41060	neural cell adhesi
53	152	9.8	1443	2 J50600	neogenesis - chicken
54	151.5	9.8	458	2 JCI509	biliary glycoprote
55	151.5	9.8	725	1 JUMSNG	neural cell adhesi
56	151.5	9.8	1115	1 JUMSNL	neural cell adhesi
57	151.5	9.8	3707	2 S18252	heparan sulfate pr
58	150.5	9.7	265	2 A55811	carcinoembryonic a
59	150.5	9.7	349	2 A34815	carcinoembryonic a
60	150.5	9.7	521	2 JCI508	biliary glycoprote
61	150.5	9.7	1033	2 S19247	cell adhesion prot
62	150.5	9.7	1501	2 T58148	protein-tyrosine-p
63	150.5	9.7	1863	2 S46217	protein-tyrosine-p
64	150	9.7	702	2 A36319	carcinoembryonic a
65	150	9.7	2783	2 J34416	hypothetical prote
66	149.5	9.7	725	2 JE0100	neural cell adhesi
67	149.5	9.7	1907	2 S50893	protein-tyrosine-p
68	149	9.7	526	1 A32164	biliary glycoprote
69	149	9.7	647	2 B41288	vascular cell adhe
70	149	9.7	739	2 A41288	vascular cell adhe
71	148.5	9.6	650	1 JCI450	fibroblast growth
72	148	9.6	1021	2 J39207	leukocyte surface
73	148	9.6	1612	2 T30805	ductal protein - mo
74	147.5	9.6	946	1 A47299	tor-related recept
75	147.5	9.6	1092	1 JN0635	neural cell adhesi
76	147	9.5	333	2 A31923	analagm protein pr
77	146.5	9.5	458	1 WMSR1	biliary glycoprote
78	146.5	9.5	1694	2 S50055	siatolodhesin - mou
79	146	9.5	1259	2 S36126	neural cell adhesi
80	146	9.5	4391	2 A38096	perlecan precursor
81	145	9.4	802	1 TVHUP4	fibroblast growth
82	145	9.4	871	1 I48697	protein-tyrosine k
83	145	9.4	881	1 I48697	protein-tyrosine k
84	145	9.4	1912	2 A56178	protein-tyrosine-p
85	144.5	9.4	341	2 JCI512	biliary glycoprote
86	144.5	9.4	1336	2 I60598	Fit-1 tyrosine kin
87	144.5	9.4	1897	1 TDHUKK	leukocyte antigen-
88	144	9.3	519	2 A44783	ecto-ATPase precu
89	144	9.3	1344	2 T14316	rig-1 protein - mo
90	144	9.3	1898	2 S46216	leukocyte antigen-
91	143	9.3	206	2 A40305	biliary glycoprote
92	143	9.3	286	2 A28313	carcinoembryonic a
93	143	9.3	509	2 JC5288	shp substrate-1 pr
94	143	9.3	513	2 JCS289	shp substrate-1 pr
95	143	9.3	1091	2 S01998	contactin precursor
96	143	9.3	1277	2 T30552	neural cell adhesi
97	143	9.3	26926	1 T38344	ctitin, cardiac mus
98	142.5	9.2	278	2 A39037	carcinoembryonic a
99	142.5	9.2	1262	1 B48758	protein-tyrosine-p
100	142.5	9.2	1496	1 B48758	protein-tyrosine-p
101	142	9.2	321	2 JH0395	biliary glycoprote
102	142	9.2	351	2 JH0396	biliary glycoprote

103	142	9.2	417	2	JH0394	biliary glycoprote	176	132	8.5	707	2	A38429	keratinocyte growt
104	142	9.2	464	2	C30127	transmembrane carc	177	132	8.5	1018	2	A54744	contactin 1 precu
105	142	9.2	976	2	T29583	hypothetical prote	178	132	8.5	1018	2	JC4711	neural adhesion pr
106	141.5	9.2	338	2	JCS519	50k glycoprotein p	179	131.5	8.5	419	2	B54312	pregnancy-specific
107	141.5	9.2	567	2	S29498	lymphocyte antigen	180	131.5	8.5	419	2	A36109	pregnancy-specific
108	141.5	9.2	626	1	A61084	myelin-associated	181	131.5	8.5	733	2	I49293	fibroblast growth
109	141.5	9.2	1651	2	T14160	transmembrane rece	182	131.5	8.5	822	2	I49289	fibroblast growth
110	141.5	9.2	1894	2	C54689	protein-tyrosine-p	183	131.5	8.5	1265	1	A37967	neural cell adhesi
111	141	9.1	882	2	J18912	receptor tyrosine	184	131.5	8.5	2029	1	TDPELK	protein-tyrosine-p
112	140.5	9.1	278	2	JC1506	biliary glycoprote	185	130.5	8.5	228	2	T22098	hypothetical prote
113	140.5	9.1	577	2	I50731	Ig heavy chain - n	186	130.5	8.5	304	1	RMCHH7	cell surface glyco
114	140.5	9.1	811	2	A41054	fasciclin II, tran	187	130.5	8.5	338	2	JC1238	opioid-binding pro
115	140.5	9.1	873	2	B41054	fasciclin II, pl-11	188	130.5	8.5	435	2	D33258	pregnancy-specific
116	140.5	9.1	1240	2	T03097	COO protein - huma	189	130.5	8.5	1011	2	T13669	neuromuculin - fr
117	140.5	9.1	1348	2	S51656	vascular endotheli	190	130	8.4	166	2	A33402	pregnancy-specific
118	140	9.1	890	1	A53743	protein-tyrosine k	191	130	8.4	520	1	S44099	brain-derived neur
119	139	9.0	1020	2	S05944	neuronal cell surf	192	129.5	8.4	309	2	I49503	B-lymphocyte activ
120	138.5	9.0	335	2	C54312	pregnancy-specific	193	129.5	8.4	332	1	RMHUPD	poliovirus recepto
121	138.5	9.0	335	2	B33251	nonspecific cross-	194	129.5	8.4	417	1	RMHUPA	poliovirus recepto
122	138	8.9	880	2	B53743	protein-tyrosine k	195	129.5	8.4	662	2	C40862	heparin-binding gr
123	138	8.9	1021	2	A57112	contactin precurs	196	129.5	8.4	822	1	TVHUPC	fibroblast growth
124	137.5	8.9	335	2	A33514	pregnancy-specific	197	129.5	8.4	822	2	B49151	fibroblast growth
125	137.5	8.9	341	2	JC1511	biliary glycoprote	198	129.5	8.4	1173	2	T25893	hypothetical prote
126	137.5	8.9	518	2	JC4024	poliovirus recepto	199	129	8.4	876	2	I49152	protein-tyrosine k
127	137.5	8.9	2295	2	C88369	protein unc-52 (im	200	129	8.4	1427	2	I51669	tumor suppressor -
128	137	8.9	582	1	BNRT3S	myelin-associated	201	128	8.3	309	2	S15674	cell surface glyco
129	137	8.9	626	2	BNRT3	myelin-associated	202	128	8.3	823	2	B35963	protein-tyrosine k
130	137	8.9	637	2	B33785	myelin-associated	203	127.5	8.3	424	2	A34595	pregnancy-specific
131	137	8.9	816	2	A49151	fibroblast growth	204	127.5	8.3	822	2	S19947	fibroblast growth
132	137	8.9	1333	2	I78875	receptor tyrosine	205	127.5	8.3	898	2	A40114	fasciclin II precu
133	137	8.9	1535	2	S46224	peroxidasin - fru1	206	127.5	8.3	1106	1	PFHUGB	platelet-derived g
134	136.5	8.8	273	2	B28928	pregnancy-specific	207	127.5	8.3	1197	2	T30581	neural cell adhesi
135	136.5	8.8	330	2	A29915	teratocarcinoma gl	208	127	8.2	353	2	S51242	heparin-binding fl
136	136.5	8.8	345	2	S03199	opioid-binding pro	209	127	8.2	416	1	A42879	advanced glycosyla
137	136.5	8.8	713	2	I50128	fibroblast growth	210	127	8.2	709	2	A35364	carnitine-lytic a
138	136.5	8.8	707	2	I19821	hypothetical prote	211	126.5	8.2	271	2	S43512	GP42/Basigin prote
139	136	8.8	1338	2	A5846	fibroblast growth	212	126.5	8.2	272	2	I48266	biliary glycoprote
140	135.5	8.8	832	2	JH0393	protein-tyrosine k	213	126.5	8.2	273	2	JX0107	basigin precursor
141	135.5	8.8	1367	2	A41288	protein-tyrosine k	214	126.5	8.2	824	2	S24108	protein-tyrosine k
142	135	8.7	235	2	S20000	Ig light chain pre	215	126.5	8.2	1232	2	T43027	neural cell adhesi
143	135	8.7	880	1	JC4166	protein-tyrosine k	216	126.5	8.2	1447	2	A54100	tumor suppressor p
144	134.5	8.7	275	2	A28928	pregnancy-specific	217	126	8.2	275	2	PS0402	basigin type III -
145	134.5	8.7	282	2	C28928	pregnancy-specific	218	126	8.2	374	2	S69339	Ig heavy chain V r
146	134.5	8.7	395	2	D43354	pregnancy-specific	219	126	8.2	475	2	S54879	pregnancy-specific
147	134.5	8.7	397	2	C43354	pregnancy-specific	220	126	8.2	789	2	T28714	hypothetical prote
148	134.5	8.7	406	2	E43354	pregnancy-specific	221	126	8.2	1355	2	T28715	hypothetical prote
149	134.5	8.7	417	2	A28277	pregnancy-specific	222	126	8.2	1356	2	JC1402	protein-tyrosine k
150	134.5	8.7	426	2	A35964	pregnancy-specific	223	125.5	8.1	398	2	S17428	interleukin-1 rece
151	134.5	8.7	818	1	S44098	brain-derived neur	224	125.5	8.1	419	2	JC4123	pregnancy-specific
152	134.5	8.7	822	1	TVMSRG	fibroblast growth	225	125.5	8.1	495	2	A55181	pregnancy-specific
153	134.5	8.7	1028	2	A53449	plasmacytoma-associ	226	125.5	8.1	821	1	TVHUP2	fibroblast growth
154	134.5	8.7	1330	2	S49010	embryonic receptor	227	125.5	8.1	1028	2	I58164	BIG-1 protein - ra
155	134.5	8.7	1880	2	T18531	tractin - medicina	228	125.5	8.1	1259	2	A43425	Neural cell adhesi
156	134	8.7	458	2	S23969	C-CAM2a protein is	229	125.5	8.1	1268	1	A39640	poliovirus recepto
157	134	8.7	588	2	I37202	cell-adhesion mole	230	125	8.1	530	2	A53437	Ig lambda chain -
158	134	8.7	588	2	I37202	B-CAM protein - hu	231	124.5	8.1	233	2	I51383	hemolin - cecropia
159	134	8.7	628	2	I38000	Lutheran blood gro	232	124.5	8.1	413	2	S65948	hemolyn - cecropia
160	134	8.7	919	2	T32541	unc-5 protein - Ca	233	124.5	8.1	769	1	ORRTGS	secretory componen
161	134	8.7	947	1	B44294	biliary glycoprote	234	124.5	8.1	819	1	TVCHFG	fibroblast growth
162	133.5	8.6	278	2	JC1507	pregnancy-specific	235	124.5	8.1	917	2	I48950	telencephalin prec
163	133.5	8.6	419	2	A33258	pregnancy-specific	236	124	8.0	682	2	A35969	heparin-binding gr
164	133.5	8.6	419	2	A33135	pregnancy-specific	237	124	8.0	769	2	S16236	fibroblast growth
165	133.5	8.6	426	2	B33258	pregnancy-specific	238	124	8.0	822	2	A45081	fibroblast growth
166	133.5	8.6	426	2	A35311	pregnancy-specific	239	124	8.0	822	2	A41194	keratinocyte growt
167	133.5	8.6	428	2	A27658	pregnancy-specific	240	123.5	8.0	182	2	I83053	keratinocyte growt
168	133.5	8.6	687	2	A49636	soluble vascular e	241	123.5	8.0	503	2	JC5287	SHP substrate-1 pr
169	133.5	8.6	729	2	A56795	fibroblast growth	242	123.5	8.0	523	2	I50478	neurolin - goldfis
170	133	8.6	428	2	I57486	pregnancy-specific	243	123.5	8.0	797	2	S38579	fibroblast growth
171	133	8.6	428	2	J50032	pregnancy-specific	244	123.5	8.0	1209	2	T42718	probable neural ce
172	133	8.6	1021	2	T42634	connectin/titin -	245	123	8.0	812	1	A36477	fibroblast growth
173	132.5	8.6	1021	2	S29840	opioid-binding cel	246	122.5	7.9	299	2	I46690	CD80 precursor - r
174	132	8.5	345	2	JC4025	opioid-binding cel	247	122.5	7.9	336	2	C27658	pregnancy-specific
175	132	8.5	345	2	JC1239	opioid-binding pro	248	122.5	7.9	424	2	B36109	pregnancy-specific

249	122.5	7.9	646	2	I38049	cell surface glyco
250	122	7.9	243	2	A53244	leukocyte antigen
251	122	7.9	1375	2	T13822	frazzled gene prot
252	122	7.9	1526	2	T13823	frazzled gene prot
253	121.5	7.9	233	2	S29577	Ig light chain - r
254	121.5	7.9	255	2	JC7593	SH2 domain-contain
255	121.5	7.9	318	2	F72171	K99 protein - vari
256	121.5	7.9	404	1	I61596	advanced glycosyla
257	121.5	7.9	1471	2	T19506	hypothetical prote
258	121	7.8	275	2	H35216	FP1 protein - low
259	121	7.8	402	2	T09062	probable advanced
260	121	7.8	818	2	T19120	hypothetical prote
261	121	7.8	822	2	B54846	fibroblast growth
262	121	7.8	1437	2	T11093	probable protein-t
263	119.5	7.7	257	2	P60401	basigin type II -
264	119.5	7.7	352	2	I77374	pregnancy-specific
265	119.5	7.7	960	1	JN0677	protein-tyrosine k
266	119	7.7	212	2	C33258	pregnancy-specific
267	118.5	7.7	352	2	T33433	hypothetical prote
268	118.5	7.7	524	2	S35341	ketlin - fruit fly
269	118	7.6	225	2	I51335	Ig lambda chain -
270	118	7.6	253	2	T15475	hypothetical prote
271	118	7.6	421	2	T46266	hypothetical prote
272	118	7.6	426	2	S09016	pregnancy-specific
273	118	7.6	620	2	JH0593	Schwann cell myeli
274	118	7.6	773	2	T46283	hypothetical prote
275	118	7.6	806	1	TVHUF3	fibroblast growth
276	118	7.6	806	2	A35963	protein-tyrosine k
277	118	7.6	814	1	A39752	fibroblast growth
278	117.5	7.6	328	2	S30444	SRP protein - huma
279	117.5	7.6	467	1	H1MSP3	poliovirus recepto
280	117.5	7.6	538	2	I68093	PRK2 delta - human
281	117.5	7.6	764	1	QRHUGS	secretory componen
282	117.5	7.6	1089	1	PFHUGA	platelet-derived g
283	117.5	7.6	1089	1	S33727	Ig lambda chain - r
284	117	7.6	232	2	S25756	CD6 precursor - r
285	117	7.6	330	2	I46691	fibroblast growth
286	117	7.6	480	2	B56182	fibroblast growth
287	117	7.6	508	2	A33378	antigen BCG1 precu
288	116.5	7.5	240	2	JL0143	probable tumor sup
289	116.5	7.5	267	2	A38442	probable tumor sup
290	116.5	7.5	361	2	PN0020	heparin-binding gr
291	116.5	7.5	800	2	A48991	fibroblast growth
292	116.5	7.5	801	2	I55363	pregnancy-specific
293	116	7.5	436	2	B51811	pregnancy-specific
294	116	7.5	475	2	I76668	fibroblast growth
295	116	7.5	705	2	S51635	aggreccan precursor
296	116	7.5	238	1	C50909	probable major tai
297	115.5	7.5	426	2	C55181	pregnancy-specific
298	115.5	7.5	426	2	B35334	pregnancy-specific
299	115.5	7.5	495	2	T25750	hypothetical prote
300	115.5	7.5	800	1	TVHUF2	fibroblast growth
301	115.5	7.5	235	2	S25749	Ig lambda chain -
302	114.5	7.4	772	2	T13078	K1A0992 protein -
303	114.5	7.4	820	2	S17295	fibroblast growth
304	114.5	7.4	336	2	S42632	Flc-18 protein pre
305	114	7.4	7160	2	B44194	poliovirus recepto
306	114	7.4	417	2	A44194	poliovirus recepto
307	114	7.4	480	2	A56182	fibroblast growth
308	114	7.4	1272	2	S26180	neurofascin - chlc
309	114	7.4	6831	2	A88852	protein unc-22 (lm
310	114	7.4	6839	2	S57242	twitclhin [smilari
311	114	7.4	727935	2	T27935	hypothetical prote
312	114	7.4	321	2	I54766	B-lymphocyte activ
313	113.5	7.4	588	2	JH0506	adhesion molecule
314	113.5	7.4	588	2	A45254	surface glycoprote
315	113.5	7.4	313	2	T28598	hypothetical prote
316	113	7.3	748	2	S41050	fibroblast growth
317	113	7.3	259	2	JC7109	SRV protein - hum
318	112.5	7.3	332	2	JN0067	pregnancy-specific
319	112.5	7.3	477	2	A34368	interferon gamma r
320	112.5	7.3	1906	1	S68235	myosin-light-chain
321	112.5	7.3				
322	112	7.3	750	2	S41051	fibroblast growth
323	112	7.3	987	2	A68746	protein C18F3.2 (l
324	112	7.3	1287	2	T30968	hypothetical prote
325	112	7.3	1450	2	A44027	16K myofibrillar
326	111.5	7.2	821	1	TVMSBK	fibroblast growth
327	111.5	7.2	3488	2	T34418	hypothetical prote
328	111	7.2	313	2	J01862	31R protein - vari
329	111	7.2	860	2	JC5702	EBB kinase activa
330	111	7.2	868	2	JC5701	EBB kinase activa
331	110.5	7.2	232	2	S17359	Ig lambda chain pr
332	110.5	7.2	233	2	S25747	Ig lambda chain -
333	110.5	7.2	738	2	A40096	platelet-endotheli
334	110.5	7.2	813	1	A49123	fibroblast growth
335	110.5	7.2	2051	2	T30938	receptor tyrosine
336	110.5	7.2	6658	2	T11931	projectin - fruit
337	110	7.1	213	2	A21177	Ig light chain pre
338	110	7.1	304	2	B88746	receptor C18F3.3 (l
339	110	7.1	1040	2	A57638	protein tyrosine
340	110	7.1	1103	2	T22889	hypothetical prote
341	109.5	7.1	353	2	G02922	MHC class I beta-G
342	109.5	7.1	413	2	A37778	hemolin precursor
343	109.5	7.1	477	1	I73631	brain-derived neur
344	109.5	7.1	618	2	T08685	hypothetical prote
345	109.5	7.1	822	1	A56853	brain-derived neur
346	109.5	7.1	954	2	I51703	c-kit-related kina
347	109.5	7.1	1052	2	B49120	protein-tyrosine k
348	109.5	7.1	1742	2	S24600	projectin - fruit
349	109	7.1	269	2	A46506	leukocyte activati
350	109	7.1	402	2	A54312	pregnancy-specific
351	108.5	7.0	233	2	JC5332	p53 specific singl
352	108.5	7.0	240	2	JC4121	pregnancy-specific
353	108.5	7.0	243	2	A37982	calcium vector pro
354	108.5	7.0	470	2	S22808	Ig heavy chain pre
355	108.5	7.0	587	1	A35104	brain-derived neur
356	108.5	7.0	476	2	JH0404	DM-GRASP precursor
357	108.5	7.0	821	1	S06943	brain-derived neur
358	108	7.0	612	2	I73633	gene trkC protein
359	108	7.0	773	1	QRBG	secretory componen
360	108	7.0	825	2	A55178	neurotrophin-3 rec
361	108	7.0	839	1	I73632	neurotrophin-3 rec
362	108	7.0	940	2	A40985	projectin - fruit
363	108	7.0	964	2	T15746	hypothetical prote
364	108	7.0	1363	1	B36182	protein-tyrosine k
365	108	7.0	1462	1	B36182	protein-tyrosine-p
366	107.5	7.0	240	2	S01299	Ok-45 membrane gly
367	107.5	7.0	584	2	I50419	s-glicerin precursor
368	107.5	7.0	764	2	A49448	irregular chlaem C
369	107.5	7.0	799	1	TVRTTB	nerve growth facto
370	107.5	7.0	2541	2	T29340	hypothetical prote
371	107	6.9	268	2	T23555	hypothetical prote
372	107	6.9	380	2	S12839	Ig heavy chain pre
373	107	6.9	829	2	JC4583	fibroblast growth
374	107	6.9	1142	2	S36845	myosin-binding pro
375	106.5	6.9	474	1	C39657	protein-tyrosine k
376	106.5	6.9	476	1	B39657	brain-derived neur
377	106.5	6.9	790	1	A39657	protein-tyrosine k
378	106.5	6.9	821	1	A39657	brain-derived neur
379	106	6.9	259	2	C85630	hypothetical prote
380	106	6.9	478	2	I53960	PRR2 alpha - human
381	106	6.9	850	2	JC5700	EBB kinase activa
382	106	6.9	1298	2	A48999	protein-tyrosine k
383	105.5	6.8	233	2	S25748	Ig lambda chain -
384	105.5	6.8	274	2	A47639	Ok-2 membrane gly
385	105.5	6.8	324	2	G43354	pregnancy-specific
386	105.5	6.8	326	2	F43354	pregnancy-specific
387	105.5	6.8	333	2	A43354	pregnancy-specific
388	105.5	6.8	335	2	H43354	pregnancy-specific
389	105.5	6.8	526	2	S70587	butyrophilin precu
390	105.5	6.8	592	2	S25705	Ig mu chain - shce
391	105.5	6.8	757	2	I45966	polymeric immunogl
392	105	6.8	253	2	A25687	H-2 class II hieto
393	105	6.8	281	2	H90853	probable major tai
394	105	6.8	310	2	JL0119	Fc gamma (Igc) rec

395	105	6.8	317	2	J10118	FC gamma (IgG) rec
396	105	6.8	351	2	B34595	pregnancy-specific
397	105	6.8	874	2	T29548	hypothetical prote
398	105	6.8	1000	2	I46521	ctitin - rabbit (fr
399	105	6.8	6805	2	S20901	ctitin - rabbit (fr
400	104.5	6.8	230	2	S49449	Ig lambda chain -
401	104.5	6.8	240	2	A41797	Ig light chain - s
402	104.5	6.8	309	2	I49522	gene B7-2 protein
403	104.5	6.8	474	2	I50830	Ig mu chain - Lepi
404	104.5	6.8	818	2	JC4058	fibroblast growth
405	104.5	6.8	824	2	S36439	fibroblast growth
406	104.5	6.8	1451	2	S42167	100K protein - hum
407	104.5	6.8	1599	2	T16210	hypothetical prote
408	104	6.7	238	2	A49633	Ig lambda-like cha
409	104	6.7	666	2	H89581	protein dim-1 (lmp
410	104	6.7	1367	1	S48478	glucan 1,4-alpha-g
411	103.5	6.7	261	2	C85681	hypothetical prote
412	103	6.7	228	2	S29575	Ig light chain - r
413	103	6.7	313	2	E90822	probable major tai
414	103	6.7	313	2	H36854	hemagglutinin - va
415	103	6.7	1088	1	PFRTGA	platelet-derived g
416	102.5	6.6	547	2	T25478	hypothetical prote
417	102	6.6	167	2	S29579	Ig light chain - r
418	102	6.6	210	2	JC4122	pregnancy-specific
419	102	6.6	336	2	JC4124	pregnancy-specific
420	102	6.6	629	2	A46500	Ly-9.2 antigen - m
421	102	6.6	999	2	I38547	novel cellular pro
422	101.5	6.6	416	2	S33473	interleukin-1 rece
423	101.5	6.6	3562	2	A47171	chondroitin sulfat
424	101	6.5	279	2	S04693	T-cell receptor de
425	101	6.5	333	2	S06946	FC gamma (IgG) rec
426	101	6.5	757	1	S48841	secretory componen
427	101	6.5	976	1	TVHUKT	protein-tyrosine k
428	101	6.5	977	2	I45877	protein-tyrosine k
429	101	6.5	1518	2	S37928	probable purine nu
430	100.5	6.5	181	2	PT0220	Ig lambda chain V-
431	100.5	6.5	233	2	S25752	Ig lambda chain -
432	100.5	6.5	249	1	A61087	myelin P0 glycopro
433	100.5	6.5	315	1	HNWZVT	hemagglutinin prec
434	100.5	6.5	735	2	S65739	basigin precursor
435	100	6.5	270	2	T16525	hypothetical prote
436	100	6.5	662	2	S57892	T cell receptor MI
437	99.5	6.4	135	2	S57892	Ig light chain C r
438	99.5	6.4	140	2	A34509	MHC class II histo
439	99.5	6.4	266	1	HLHJ3D	Ig lambda chain -
440	99	6.4	226	2	S25745	major tail protein
441	99	6.4	238	2	D90876	probable tail comp
442	99	6.4	262	2	C85692	neurotrophin-3 rec
443	99	6.4	825	1	A40026	Ig lambda chain pr
444	98.5	6.4	235	2	S05270	OK-2 membrane gly
445	98.5	6.4	278	1	TDRTOX	adhesive plaque pr
446	98.5	6.4	473	2	A56175	intercellular adhe
447	98.5	6.4	544	2	JC5018	fibroblast growth
448	98.5	6.4	729	2	A49120	protein kinase TMK
449	98.5	6.4	942	1	J01674	vascular endotheli
450	98.5	6.4	1379	2	JC4954	hypothetical prote
451	98.5	6.4	1398	2	T25568	MHC class I protei
452	98	6.3	176	2	I50016	Ig lambda chain V
453	98	6.3	213	2	S21066	Ig lambda chain -
454	98	6.3	235	2	S25754	B16R protein - vac
455	98	6.3	230	2	F42527	macrophage colony-
456	98	6.3	980	1	TVCTMD	receptor tyrosine
457	98	6.3	983	2	B45563	myosin-binding pro
458	98	6.3	1123	2	S36846	myosin-binding pro
459	98	6.3	1138	2	S24614	Ig lambda chain (N
460	97.5	6.3	208	2	B49444	Ig lambda chain -
461	97.5	6.3	235	2	S25750	MHC class II histo
462	97.5	6.3	266	1	HLHJ4D	nephlin - human
463	97.5	6.3	1241	2	T37190	cell adhesion mole
464	97	6.3	261	2	I48645	FC gamma (IgG) rec
465	97	6.3	330	2	A40071	FC-gamma-1/gamma-2
466	97	6.3	330	2	I49660	aggreccan - pig (fr
467	97	6.3	370	2	S29139	
468	97	6.3	487	2	T28804	hypothetical prote
469	97	6.3	504	2	S00390	Ig gamma chain (cl
470	96.5	6.2	216	2	S29258	Ig lambda chain V
471	96.5	6.2	233	2	S25744	Ig lambda chain -
472	96.5	6.2	283	1	FCMSG1	FC gamma (IgG) rec
473	96.5	6.2	288	2	A45803	B-cell-restricted
474	96.5	6.2	978	2	S16385	macrophage colony-
475	96.5	6.2	1051	2	A12316	hypothetical prote
476	96.5	6.2	1225	1	S24284	B2 glycoprotein pr
477	96.5	6.2	1225	1	S46607	B2 glycoprotein -
478	96.5	6.2	1449	1	VG1HFS	B2 glycoprotein pr
479	96	6.2	152590	2	I52590	m33-B isoform - mo
480	96	6.2	416	2	T50279	hypothetical serin
481	96	6.2	473	2	D88976	protein F5A42.4 [i
482	96	6.2	583	2	I39428	album - human
483	96	6.2	856	2	I58411	protein-tyrosine k
484	96	6.2	976	1	TVMSGD	macrophage colony-
485	96	6.2	1147	2	A59307	myosin-light-chain
486	96	6.2	1666	2	A48594	ekelamin - mouse
487	95.5	6.2	224	2	S25757	Ig lambda chain -
488	95.5	6.2	249	2	S41374	single chain Fv an
489	95.5	6.2	499	2	S33766	platelet-derived g
490	95.5	6.2	1200	2	T43148	probable protein-c
491	95.5	6.2	1274	2	S55050	cardiac myosin-bi
492	95.5	6.2	1465	2	S43529	165K protein, ekel
493	95	6.2	282	2	T17219	hypothetical prote
494	95	6.2	466	2	UC5897	killer cell inhibi
495	95	6.2	572	2	B46529	Ig y heavy chain (
496	95	6.2	817	2	A48721	ctitin, muscle - ch
497	95	6.2	941	1	TVVMVD	protein-tyrosine k
498	95	6.2	2124	2	A28452	aggreccan precursor
499	95	6.2	2132	1	A55182	aggreccan precursor
500	95	6.2	2415	1	A39086	Ig lambda chain (K
501	94.5	6.1	216	2	S03401	Ig lambda chain -
502	94.5	6.1	233	2	S25741	T-cell receptor be
503	94.5	6.1	267	2	PL0064	cell surface glyco
504	94.5	6.1	335	2	A53434	MHC class I histoc
505	94.5	6.1	358	2	A28834	platelet-derived g
506	94.5	6.1	1098	1	PFMSRB	B2 glycoprotein pr
507	94.5	6.1	1449	1	A43573	Ig heavy chain pre
508	94	6.1	144	1	AVMS67	Ig lambda chain -
509	94	6.1	236	2	S25746	Ig heavy chain pre
510	94	6.1	344	2	I54445	MHC H2-0a-Mb1 - m
511	94	6.1	432	2	P86639	protein-C34H4.3 [
512	94	6.1	975	1	TVMSKT	protein-tyrosine k
513	94	6.1	1177	2	T16594	hypothetical prote
514	93.5	6.1	154	2	S21649	T-cell receptor be
515	93.5	6.1	254	2	C42691	fibroblast growth
516	93.5	6.1	266	1	HLHJ1B	MHC class II histo
517	93.5	6.1	302	2	I56072	MHC class II HLA-D
518	93.5	6.1	326	2	C36464	fibroblast growth
519	93.5	6.1	326	1	WMVZ15	B15R protein precu
520	93	6.0	281	2	E85843	hypothetical prote
521	93	6.0	314	1	HNWZVM	hemagglutinin prec
522	93	6.0	314	1	J01793	hemagglutinin prec
523	93	6.0	2327	2	T42630	aggreccan - bovine
524	92.5	6.0	213	2	UE0247	Ig lambda chain NI
525	92.5	6.0	266	1	HLHJWB	MHC class II histo
526	92.5	6.0	326	2	T37450	interleukin-1 beta
527	92.5	6.0	345	2	A46052	vascular cell adhe
528	92.5	6.0	701	2	T17243	hypothetical prote
529	92.5	6.0	1327	2	T09402	immunoglobulin-11k
530	92	6.0	217	2	B25687	H-2 class II histo
531	92	6.0	231	2	S25753	Ig lambda chain -
532	92	6.0	274	2	S33440	T-cell receptor ga
533	92	6.0	310	1	HNWZRA	hemagglutinin prec
534	92	6.0	568	2	A34891	Ig heavy chain pre
535	92	6.0	771	2	D49423	gemaphorin III pre
536	92	6.0	2256	2	AD1018	large repetitive p
537	91.5	5.9	229	2	A20969	Ig kappa chain pre
538	91.5	5.9	235	2	S25058	Ig kappa chain - m
539	91.5	5.9	289	2	G00031	B7 protein - red-c
540	91.5	5.9	348	2	I68745	MHC class I lympho

541	91.5	5.9	358	2	B87063	conserved hypother	614	89	5.8	1679	2	T30271	surface protein -
542	91.5	5.9	391	2	S72717	Lebpb170_P3_112 pr	615	89	5.8	1691	1	D54689	protein-tyrosine-p
543	91.5	5.9	368	2	A45804	Ig mu chain C regi	616	89	5.8	1381	2	T42389	versican precursor
544	91.5	5.9	573	2	S12838	Ig mu chain precu	617	89	5.8	13055	2	T16580	hypothetical prote
545	91.5	5.9	619	2	T15669	hypothetical prote	618	88.5	5.7	128	2	S24319	Ig lambda chain pr
546	91.5	5.9	625	2	T16777	hypothetical prote	619	88.5	5.7	182	2	A28508	T-cell surface gly
547	91.5	5.9	684	2	S60266	novel antigen rece	620	88.5	5.7	186	2	161783	sodium channel bet
548	91.5	5.9	1048	2	T30815	platelet-derived g	621	88.5	5.7	265	2	B39797	MHC class II histo
549	91	5.9	117	2	E33989	Ig heavy chain V-5	622	88.5	5.7	348	2	S09273	Ig alpha chain C r
550	91	5.9	202	2	S36293	T-cell receptor ga	623	88.5	5.7	356	2	A27797	class I histocompa
551	91	5.9	237	2	C27060	class II histocomp	624	88.5	5.7	680	2	JC5895	killer cell inhibi
552	91	5.9	240	2	A39016	T-cell surface gly	625	88.5	5.7	902	2	E90212	conserved hypother
553	91	5.9	266	2	I54287	gene HLA-DRB1 prot	626	88.5	5.7	1578	2	AD1512	peptidoglycan bou
554	91	5.9	266	2	A27618	class II histocomp	627	88	5.7	220	2	A49444	Ig gamma-1 heavy c
555	91	5.9	1649	2	C68822	hypothetical prote	628	88	5.7	234	2	S14237	Ig kappa chain pre
556	91	5.9	2380	2	T29551	hypothetical prote	629	88	5.7	241	2	D43273	heregulin precursor
557	91	5.9	2468	2	A83412	hypothetical prote	630	88	5.7	270	2	A34636	Fc-gamma receptor
558	91	5.9	5147	1	IJFFM	cadherin-related t	631	88	5.7	348	2	A56247	natural killer cel
559	90.5	5.9	162	2	I51668	tumor suppressor -	632	88	5.7	376	2	T48950	cyteine proteinas
560	90.5	5.9	175	2	T01365	probable prolins-r	633	88	5.7	405	2	S33601	cell adhesion mole
561	90.5	5.9	178	2	S29594	Ig gamma chain (W	634	88	5.7	451	2	T30603	perlecan homolog
562	90.5	5.9	232	2	S25742	Ig lambda chain -	635	88	5.7	462	2	I38404	neu differentiatio
563	90.5	5.9	233	2	JH0372	42k surface glycop	636	88	5.7	637	2	C43273	heregulin precursor
564	90.5	5.9	241	2	S32359	glial growth facto	637	88	5.7	645	2	B43273	heregulin, splice
565	90.5	5.9	251	2	T15485	hypothetical prote	638	88	5.7	974	2	A49714	protein-tyrosine k
566	90.5	5.9	266	2	A25324	class II histocomp	639	88	5.7	1005	2	T18537	Ig heavy chain - c
567	90.5	5.9	266	2	I54448	MHC class II histo	640	87.5	5.7	104	1	K5RBY	Ig kappa chain C r
568	90.5	5.9	268	2	A56446	Ig heavy chain V r	641	87.5	5.7	141	2	S31702	Ig heavy chain V r
569	90.5	5.9	315	1	HNWZV	hemagglutinin prec	642	87.5	5.7	237	2	H28043	MHC class II histo
570	90.5	5.9	315	2	T37438	hemagglutinin - va	643	87.5	5.7	264	2	A60497	H-2 class II histo
571	90.5	5.9	937	2	A45082	neurotrophic recep	644	87.5	5.7	307	2	S5556	hypothetical prote
572	90.5	5.9	1176	2	JN0583	myosin-light-chain	645	87.5	5.7	362	2	G02426	interleukin-1 rece
573	90.5	5.9	1449	2	S47423	E2 glycoprotein pr	646	87.5	5.7	694	2	C83826	penicillin-binding
574	90.5	5.8	116	2	S22556	Ig heavy chain V r	647	87.5	5.7	1999	2	AB2018	hypothetical prote
575	90	5.8	231	2	S25751	Ig lambda chain -	648	87.5	5.7	2383	2	D64962	probable membrane
576	90	5.8	323	2	A48997	tumor surface anti	649	87.5	5.7	2409	1	A60979	versican precursor
577	90	5.8	335	2	S09275	Ig alpha chain C r	650	87.5	5.7	4936	2	AH2515	hypothetical prote
578	90	5.8	338	2	I49443	gene 284 protein -	651	87	5.6	137	2	C45883	T-cell receptor al
579	90	5.8	409	2	T33019	hypothetical prote	652	87	5.6	164	2	T17995	hypothetical prote
580	90	5.8	531	2	B88109	protein T24E12.5 f	653	87	5.6	228	2	JC7761	dendritic cell-der
581	90	5.8	661	2	G82985	probable choline t	654	87	5.6	237	2	G28043	MHC class II histo
582	90	5.8	749	2	G01856	semaphorin V - hum	655	87	5.6	357	2	I67482	MHC class I heavy
583	90	5.8	894	1	A41527	protein-tyrosine k	656	87	5.6	510	2	PC4054	cardiac C-protein
584	90	5.8	1471	2	B48218	neurexin III-alpha	657	87	5.6	570	2	A57535	interleukin 1 recep
585	89.5	5.8	104	2	F53275	Ig kappa-1 chain C	658	87	5.6	2660	2	B85822	probable invasin Z
586	89.5	5.8	267	2	I72882	Fc gamma receptor	659	86.5	5.6	103	2	B26167	Ig lambda chain C
587	89.5	5.8	307	1	RWMSBC	T-cell receptor be	660	86.5	5.6	135	2	S10004	hypothetical prote
588	89.5	5.8	315	1	HNWZAX	hemagglutinin prec	661	86.5	5.6	142	1	EVRRP2	Ig heavy chain pre
589	89.5	5.8	329	2	A40730	class I histocompa	662	86.5	5.6	151	2	PL0011	Ig heavy chain pre
590	89.5	5.8	422	2	S32357	glial growth facto	663	86.5	5.6	166	2	PL0012	Ig heavy chain pre
591	89.5	5.8	505	2	B46629	mucin 6, galectic (664	86.5	5.6	216	2	A42193	Ig lambda chain (B
592	89.5	5.8	531	2	S20900	cltin - mouse (fra	665	86.5	5.6	230	2	A56210	neu differentiatio
593	89.5	5.8	599	2	T16774	hypothetical prote	666	86.5	5.6	235	2	S25758	Ig lambda chain -
594	89.5	5.8	692	2	G90284	hypothetical prote	667	86.5	5.6	235	2	S14675	Ig lambda chain -
595	89.5	5.8	767	1	UT0474	glucan 1,4-alpha-g	668	86.5	5.6	240	2	S06084	Ig kappa chain pre
596	89.5	5.8	778	1	ALBYG	glucan 1,4-alpha-g	669	86.5	5.6	266	2	B27618	MHC class II histo
597	89.5	5.8	1014	2	T24412	hypothetical prote	670	86.5	5.6	266	2	A45856	Ig gamma-1 chain C
598	89.5	5.8	1345	2	H90975	hypothetical prote	671	86.5	5.6	330	1	GHHU	Ig alpha chain C r
599	89.5	5.8	1526	2	T19473	hypothetical prote	672	86.5	5.6	343	2	S09272	butyrophilin - mou
600	89.5	5.8	3083	2	AH2493	hypothetical prote	673	86.5	5.6	487	2	S65133	glycoprotein C - h
601	89	5.8	182	2	A34647	pregnancy-specific	674	86.5	5.6	511	1	VGBB1K	Ig heavy chain, be
602	89	5.8	215	2	A57843	sodium channel bet	675	86.5	5.6	580	2	A46538	neu differentiatio
603	89	5.8	225	2	S37484	Ig kappa chain - m	676	86.5	5.6	636	2	I61718	neu differentiatio
604	89	5.8	266	2	I54295	lymphocyte antigen	677	86.5	5.6	639	2	161719	neu differentiatio
605	89	5.8	309	2	S18894	T-cell receptor be	678	86.5	5.6	662	2	I61722	polynucleotide pho
606	89	5.8	368	2	T24408	hypothetical prote	679	86.5	5.6	719	2	F82831	semaphorin E - mou
607	89	5.8	454	2	A46532	Ig mu chain C regi	680	86.5	5.6	751	2	I48748	mucin-like glycopr
608	89	5.8	459	2	A46254	Cd4 precursor - ra	681	86.5	5.6	1832	2	T31113	Ig heavy chain V r
609	89	5.8	459	2	C69377	conserved hypother	682	86	5.6	125	2	S68170	T-cell surface gly
610	89	5.8	640	2	A43273	heregulin precursor	683	86	5.6	210	2	S25657	signaling lymphocy
611	89	5.8	818	1	A30107	deipeptidyl aminope	684	86	5.6	335	2	S58892	glycoprotein VI-1
612	89	5.8	994	2	T49276	c-met tyrosine kin	685	86	5.6	339	2	JC7509	T-cell surface gly
613	89	5.8	1643	2	T14274	versican precursor	686	86	5.6	347	2	S41638	

687	86	5.6	362	2	A45845	MHC class I histoc	760	83.5	5.4	476	2	T25736	hypothetical prote
688	86	5.6	367	2	T12790	N-acetylglucosyl-L	761	83.5	5.4	627	2	S14683	Ig mu chain precu
689	86	5.6	416	2	A54017	colon carcinoma-as	762	83.5	5.4	975	2	T48974	receptor-protein c
690	86	5.6	545	2	U00341	intercellular adhe	763	83.5	5.4	1495	2	T31434	denasin-180 - rat
691	86	5.6	983	2	T30816	macrophage colony-	764	83.5	5.4	1810	1	A42230	tenascin precursor
692	86	5.6	975	2	A45583	receptor tyrosine	765	83.5	5.4	3033	1	Q01303	genome polypeptor
693	85.5	5.5	178	2	A45583	Ig kappa chain V-C	766	83	5.4	119	2	PS0091	Ig heavy chain V r
694	85.5	5.5	221	2	S49220	Ig gamma-1 chain -	767	83	5.4	149	2	S30752	Ig heavy chain pre
695	85.5	5.5	266	2	A28031	MHC class II histoc	768	83	5.4	200	2	D32526	class II histocomp
696	85.5	5.5	266	2	I54509	MHC class II HLA-D	769	83	5.4	247	2	I50465	MHC class II beta
697	85.5	5.5	277	2	I52825	gene MAC25 protein	770	83	5.4	354	2	I69002	histocompatibility
698	85.5	5.5	282	2	S50031	prostaglandin-simu	771	83	5.4	358	2	B75197	hypothetical prote
699	85.5	5.5	303	2	A40807	membrane glycopro	772	83	5.4	398	2	A37274	glycine-derived nexin
700	85.5	5.5	400	2	T34363	hypothetical prote	773	83	5.4	426	2	B53580	neurexin III beta
701	85.5	5.5	403	2	B69589	argininosuccinate	774	83	5.4	525	1	A58574	neurotrophin-3 rec
702	85.5	5.5	473	1	MHDM	Ig mu chain C regi	775	83	5.4	537	2	A46611	myosin-binding pro
703	85.5	5.5	772	2	A49069	collapsin - chickc	776	83	5.4	537	2	G85021	protoporphyrinogen
704	85.5	5.5	1181	2	A33998	integrin alpha-2 c	777	83	5.4	803	1	S35695	neurotrophin-3 rec
705	85.5	5.5	1715	2	JB0128	Bombay mori recept	778	83	5.4	852	2	I51259	tyrosine kinase C
706	85	5.5	117	2	S22552	Ig heavy chain V r	779	83	5.4	933	2	A31930	cytoactin - chick
707	85	5.5	121	2	H36005	Ig heavy chain V r	780	83	5.4	977	2	S49004	tyrosine kinase Mp
708	85	5.5	197	2	S29593	Ig kappa chain (MM	781	83	5.4	1036	2	T30311	S-layer protein -
709	85	5.5	265	2	C39797	MHC class II histo	782	82.5	5.3	105	2	PH0978	Ig heavy chain V r
710	85	5.5	269	2	I51540	MHC class II beta-	783	82.5	5.3	129	2	B30598	T-cell receptor be
711	85	5.5	327	1	G4HU	Ig gamma-4 chain C	784	82.5	5.3	237	2	F27060	class II histocomp
712	85	5.5	1456	2	G86466	hypothetical prote	785	82.5	5.3	248	1	MPPR0	myelin P0 protein
713	85	5.5	1477	2	T13797	tumor suppressor pr	786	82.5	5.3	261	2	E39797	MHC class II DR-be
714	85	5.5	1939	2	D97316	probable S-layer p	787	82.5	5.3	266	2	A39797	MHC class II histo
715	85	5.5	2233	2	B95075	beta-galactosidase	788	82.5	5.3	326	1	G2HU	Ig gamma-2 chain C
716	85	5.5	3191	2	T22945	hypothetical prote	789	82.5	5.3	362	1	HLHDB8	MHC class I histoc
717	84.5	5.5	112	2	PL0232	Ig heavy chain V r	790	82.5	5.3	395	2	I77371	CD445 - human
718	84.5	5.5	132	2	A24402	T-cell receptor al	791	82.5	5.3	408	1	LKRR2	proteoglycan link
719	84.5	5.5	225	2	T10029	Ig kappa chain pre	792	82.5	5.3	419	2	AH3166	hypothetical prote
720	84.5	5.5	355	2	D72174	DR protein - vari	793	82.5	5.3	432	1	RMQGT4	T-cell surface gly
721	84.5	5.5	375	2	I60125	PDGF receptor beta	794	82.5	5.3	436	2	T00756	hypothetical prote
722	84.5	5.5	381	2	I51174	Ig heavy chain - R	795	82.5	5.3	569	2	A36187	interleukin-1 rece
723	84.5	5.5	398	2	A39371	Ig V-region-like B	796	82.5	5.3	609	2	G87496	peptidase, M23/M37
724	84.5	5.5	438	1	HVRKCS	Ig mu chain C regi	797	82.5	5.3	719	2	S63629	homeotic protein A
725	84.5	5.5	448	2	A46533	Ig heavy chain C r	798	82.5	5.3	775	2	S63626	homeotic protein A
726	84.5	5.5	457	2	S03961	Ig mu chain C regi	799	82.5	5.3	812	2	TS2569	squamosa-promoter
727	84.5	5.5	461	1	HVRKCO	Ig mu chain C regi	800	82.5	5.3	826	2	B55363	desmocollin, type
728	84.5	5.5	526	1	A37821	butyrophilin - bov	801	82.5	5.3	894	2	T27007	hypothetical prote
729	84.5	5.5	705	2	AC0424	polyribonucleotide	802	82.5	5.3	896	2	A55363	desmocollin, type
730	84.5	5.5	1797	2	T21889	hypothetical prote	803	82.5	5.3	914	2	C69284	surface layer prot
731	84.5	5.5	1805	2	T21888	hypothetical prote	804	82.5	5.3	1035	2	G86342	hypothetical prote
732	84.5	5.5	2228	2	E97942	beta-galactosidase	805	82.5	5.3	1200	2	T17404	hyalini - sea urchi
733	84	5.4	98	2	G47624	Ig heavy chain V-V	806	82.5	5.3	1530	2	AH1396	peptidoglycan anch
734	84	5.4	145	2	I46633	rearranged T-cell	807	82	5.3	102	2	B34509	Ig light chain C r
735	84	5.4	155	2	A41675	relonkin - rabbit	808	82	5.3	119	2	S24683	Ig heavy chain V6
736	84	5.4	220	2	G90290	hypothetical prote	809	82	5.3	135	2	S40342	Ig kappa chain - h
737	84	5.4	226	2	A53273	MHC class II histo	810	82	5.3	146	2	S02083	Ig lambda chain V-
738	84	5.4	231	2	S25738	Ig lambda chain -	811	82	5.3	230	2	S33161	Ig kappa chain - B
739	84	5.4	234	2	A39956	Ig lambda chain pr	812	82	5.3	249	2	I50464	MHC class II beta
740	84	5.4	237	2	I54294	MHC HLA-DR-beta su	813	82	5.3	269	2	I51542	MHC class II beta-
741	84	5.4	242	2	S25663	T-cell surface gly	814	82	5.3	269	2	I51539	MHC class II beta-
742	84	5.4	247	1	A54662	myelin P0 protein	815	82	5.3	289	2	S01441	class II histocomp
743	84	5.4	321	2	S10006	hypothetical prote	816	82	5.3	350	2	I50015	MHC class I protei
744	84	5.4	352	2	S09286	Ig alpha chain C r	817	82	5.3	352	2	S76078	streptogramin lyas
745	84	5.4	359	2	I61867	MHC class I protei	818	82	5.3	367	1	MHCH	Ig mu chain C regi
746	84	5.4	452	1	MHNU	Ig mu chain C regi	819	82	5.3	531	2	S06016	intercellular adhe
747	84	5.4	472	2	S31459	Ig gamma-1 chain -	820	82	5.3	537	2	I49769	intercellular adhe
748	84	5.4	498	2	D86298	hypothetical prote	821	82	5.3	537	2	A45815	intercellular adhe
749	84	5.4	602	2	A45769	acetylcholine rece	822	82	5.3	545	2	T02005	protoporphyrinogen
750	84	5.4	794	2	I59372	cadherin 12 - huma	823	82	5.3	743	2	T42557	tegument protein I
751	84	5.4	893	2	H82543	DNA gyrase subunit	824	82	5.3	764	2	S50878	hypothetical prote
752	84	5.4	1054	2	JC7294	alpha integrin -	825	82	5.3	811	2	PN0689	connectin 1 - chic
753	84	5.4	1227	2	C97033	uncharacterized pr	826	82	5.3	1132	2	A35089	myosin-binding pro
754	84	5.4	2109	2	E89066	protein H05009.1 l	827	82	5.3	3507	2	T34513	hypothetical prote
755	84	5.4	2109	2	T33247	hypothetical prote	828	81.5	5.3	111	2	PH1573	T-cell receptor be
756	83.5	5.4	246	2	I59092	HLA-DR beta-chain	829	81.5	5.3	121	2	A30551	Ig heavy chain V r
757	83.5	5.4	332	2	G83458	sulfate-binding pr	830	81.5	5.3	139	2	E27639	T-cell receptor ga
758	83.5	5.4	354	2	I54551	histocompatibility	831	81.5	5.3	144	2	B40098	colorectal cancer
759	83.5	5.4	364	2	A30551	myeloid cell surfa	832	81.5	5.3	212	2	S70431	Ig lambda chain -

833	81.5	5.3	270	2	151543	MHC class II beta-
834	81.5	5.3	285	2	S36903	Fc gamma (IgG) rec
835	81.5	5.3	305	2	S07115	class I histocompa
836	81.5	5.3	308	2	I36956	MHC CnIIa chain - C
837	81.5	5.3	354	2	I80170	class I histocompa
838	81.5	5.3	354	2	S46877	B20R protein - var
839	81.5	5.3	354	2	T28616	hypothetical prote
840	81.5	5.3	354	2	S24438	class I histocompa
841	81.5	5.3	354	2	S24440	class I histocompa
842	81.5	5.3	358	2	S03538	class I histocompa
843	81.5	5.3	359	1	HLHUB4	MHC class I histoc
844	81.5	5.3	362	1	HLHUB7	MHC class I histoc
845	81.5	5.3	362	1	HLHUB7	MHC class I histoc
846	81.5	5.3	362	2	I64488	MHC class I protei
847	81.5	5.3	362	2	I64488	lymphocyte antigen
848	81.5	5.3	362	2	I54505	lymphocyte antigen
849	81.5	5.3	362	2	I54314	MHC HLA-B39N - hum
850	81.5	5.3	362	2	S60601	HLA-BPOT (classII)
851	81.5	5.3	362	2	I59645	HLA-B-6701 - human
852	81.5	5.3	362	2	I69850	MHC class I histoc
853	81.5	5.3	362	2	I61903	MHC class I histoc
854	81.5	5.3	362	2	I61859	MHC HLA-B14 chain
855	81.5	5.3	362	2	I59651	lymphocyte antigen
856	81.5	5.3	365	2	I56053	class I histocompa
857	81.5	5.3	492	2	A97429	flk protein prote
858	81.5	5.3	492	2	A82647	hook associated pr
859	81.5	5.3	578	2	I41715	hypothetical prote
860	81.5	5.3	790	1	T4VHUT7	nerve growth facto
861	81.5	5.3	842	2	T04555	hypothetical prote
862	81.5	5.3	896	2	I45858	desmocollin - bovi
863	81.5	5.3	953	2	C69824	hypothetical prote
864	81.5	5.3	978	1	A49814	protein-tyrosine k
865	81.5	5.3	1389	2	T47796	ABC transporter-11
866	81.5	5.3	1559	1	S64572	probable membrane
867	81	5.2	119	2	A24672	Ig heavy chain pre
868	81	5.2	127	2	S70444	Ig lambda chain pr
869	81	5.2	143	2	PT0174	Ig heavy chain pre
870	81	5.2	144	2	I46642	rearranged T-cell
871	81	5.2	196	2	T19794	hypothetical prote
872	81	5.2	210	2	E46482	T-cell surface gly
873	81	5.2	214	2	PC4156	Ig lambda chain V
874	81	5.2	217	2	T80246	Ig lambda chain NI
875	81	5.2	221	2	C46482	T-cell surface gly
876	81	5.2	237	2	E28043	MHC class II histc
877	81	5.2	246	2	T01073	T cell surface gly
878	81	5.2	247	2	I50093	MHC class II beta
879	81	5.2	252	2	A46505	SLA-DRAD (MHC clas
880	81	5.2	266	2	A29310	MHC class II histc
881	81	5.2	321	2	A71510	hypothetical prote
882	81	5.2	351	1	SAVZV	surface antigen pr
883	81	5.2	378	2	I46268	brevican precursor
884	81	5.2	426	2	I36948	Ig epsilon-chain -
885	81	5.2	454	1	MEHY	Ig mu chain C regi
886	81	5.2	631	2	I52257	epistatin - mouse
887	81	5.2	666	1	JE0201	protein-tyrosine k
888	81	5.2	666	1	I58169	semaphorin A - mou
889	81	5.2	748	2	I48744	semaphorin A - mou
890	81	5.2	942	2	T20287	hypothetical prote
891	81	5.2	943	2	B45082	neurotrophic recep
892	81	5.2	983	2	A38224	protein-tyrosine k
893	81	5.2	1146	2	S46837	hypothetical prote
894	81	5.2	1747	2	A45974	collagen alpha 1(X
895	81	5.2	1827	2	T34288	hypothetical prote
896	81	5.2	1902	2	S06997	lactocepin (BC 3.4
897	81	5.2	1902	2	B45764	lactocepin (BC 3.4
898	81	5.2	3343	2	T42207	breast cancer auc
899	80.5	5.2	105	2	B30554	Ig lambda chain C
900	80.5	5.2	139	2	T27639	T-cell receptor ga
901	80.5	5.2	215	2	JE0243	Ig kappa chain NI
902	80.5	5.2	251	2	I18053	myelin protein zer
903	80.5	5.2	264	2	S10989	class II histocomp
904	80.5	5.2	264	2	I46020	Fc gamma 2 recepto
905	80.5	5.2	290	2	AG2216	hypothetical prote
906	80.5	5.2	338	2	I56116	MHC HLA-B27-HS - h
907	80.5	5.2	350	2	I68747	MHC class I lympho
908	80.5	5.2	354	2	I80155	class I histocompa
909	80.5	5.2	355	2	T28119	MHC class I histoc
910	80.5	5.2	361	2	I54418	MHC class I histoc
911	80.5	5.2	361	1	HLHUB2	MHC class I histoc
912	80.5	5.2	362	2	I37492	HLA-B alpha-chain
913	80.5	5.2	362	2	S52486	HLA-B protein alph
914	80.5	5.2	362	2	I56119	lymphocyte antigen
915	80.5	5.2	362	2	A45850	MHC class I histoc
916	80.5	5.2	362	2	I61864	MHC HLA-Bw41 chain
917	80.5	5.2	362	2	I61906	MHC class I histoc
918	80.5	5.2	362	2	I59655	lymphocyte antigen
919	80.5	5.2	362	2	I84431	MHC HLA-B8 chain -
920	80.5	5.2	362	2	I61905	MHC class I histoc
921	80.5	5.2	362	2	I54442	MHC class I histoc
922	80.5	5.2	362	2	I61865	MHC HLA-Bw42, HLA-
923	80.5	5.2	364	2	D35997	MHC class I histoc
924	80.5	5.2	476	2	T27618	hypothetical prote
925	80.5	5.2	605	2	S67815	protein-tyrosine k
926	80.5	5.2	656	2	S49745	probable membrane
927	80.5	5.2	661	2	E71427	hypothetical prote
928	80.5	5.2	706	2	H81943	probable polyribon
929	80.5	5.2	707	2	C81161	polyribonucleotide
930	80.5	5.2	834	2	T42702	hypothetical prote
931	80.5	5.2	936	1	S64384	probable membrane
932	80.5	5.2	1134	1	UN0711	protein-tyrosine k
933	80.5	5.2	2123	2	F86348	hypothetical prote
934	80.5	5.2	2626	2	T31099	myosin-RhoGAP prot
935	80.5	5.2	118	2	S18556	Ig heavy chain V r
936	80	5.2	133	2	PH1286	Ig heavy chain pre
937	80	5.2	144	2	PH1285	Ig lambda chain -
938	80	5.2	190	2	S25740	protein T2211.8 (
939	80	5.2	233	2	A86344	class II histocomp
940	80	5.2	243	2	A60472	probable fibribrial
941	80	5.2	245	2	S29980	class II histocomp
942	80	5.2	246	2	D46482	T-cell surface gly
943	80	5.2	266	1	HLHUSD	MHC class II histc
944	80	5.2	266	2	D39797	MHC class II histc
945	80	5.2	333	2	T27883	hypothetical prote
946	80	5.2	334	1	RWRTC2	T-cell surface gly
947	80	5.2	353	1	SAVZVC	surface antigen pr
948	80	5.2	393	1	HYRXC1	Ig mu chain C regi
949	80	5.2	432	1	RKCZT4	T-cell surface gly
950	80	5.2	458	1	RWHUT4	T-cell surface gly
951	80	5.2	484	2	C88264	protein kin-15 (im
952	80	5.2	488	2	I44330	protein-tyrosine k
953	80	5.2	536	2	T37544	hypothetical serin
954	80	5.2	576	2	T40476	hypothetical prote
955	80	5.2	615	2	UC7576	transcription fact
956	80	5.2	654	2	T19785	hypothetical prote
957	80	5.2	708	2	AG2315	hypothetical prote
958	80	5.2	749	2	E86774	hypothetical prote
959	80	5.2	888	2	S23065	uto protein - mous
960	80	5.2	942	2	S23251	protein-tyrosine k
961	80	5.2	1053	2	I55534	VIA-3 alpha subun
962	80	5.2	1081	2	S51899	probable protein k
963	80	5.2	1185	2	T46428	hypothetical prote
964	80	5.2	1537	2	S53465	floucculation prote
965	80	5.2	1848	2	A44140	cellulose-binding
966	79.5	5.1	119	1	L1PG	Ig lambda chain C
967	79.5	5.1	119	2	S18555	Ig heavy chain V r
968	79.5	5.1	119	2	C33876	carcinoembryonic
969	79.5	5.1	120	2	A32072	Ig heavy chain pre
970	79.5	5.1	131	2	T20334	hypothetical prote
971	79.5	5.1	136	2	B45893	T-cell receptor al
972	79.5	5.1	138	2	A26471	Ig kappa chain pre
973	79.5	5.1	156	2	T05849	hypothetical prote
974	79.5	5.1	245	2	I55951	MHC class II E-bet
975	79.5	5.1	253	2	T49416	hypothetical prote
976	79.5	5.1	257	2	S29981	class II histocomp
977	79.5	5.1	260	2	I51544	MHC class II beta-
978	79.5	5.1	267	2	A35902	Fc gamma (IgG) rec

979	79.5	5.1	284	2	509769	hypothetical prote	1052	79	5.1	267	2	156110	Fe-gamma RIIIB- α p
980	79.5	5.1	291	2	A70475	H α -transporting tw	1053	79	5.1	333	2	PS0018	Ig gamma-2b chain
981	79.5	5.1	304	2	A65198	hypothetical prote	1054	79	5.1	351	1	SAVZWR	surface antigen pr
982	79.5	5.1	325	2	T36434	lysine ammonia-	1055	79	5.1	335	2	B40730	class I histocompa
983	79.5	5.1	325	2	T03010	probable replicati	1056	79	5.1	376	2	E85435	cysteine peroxi
984	79.5	5.1	327	2	AF0618	conserved hypochet	1057	79	5.1	421	2	T10190	L-ascorbate peroxi
985	79.5	5.1	335	2	A87135	probable membrane	1058	79	5.1	430	2	H72604	hypothetical prote
986	79.5	5.1	354	2	S24433	class I histocompa	1059	79	5.1	479	1	VGBEF2	glycoprotein F - h
987	79.5	5.1	354	2	S24436	class I histocompa	1060	79	5.1	492	2	AH1030	probable exported
988	79.5	5.1	354	2	S24437	class I histocompa	1061	79	5.1	556	2	F83421	glutaminyl-t-RNA sy
989	79.5	5.1	360	2	S09271	Ig alpha chain C r	1062	79	5.1	623	2	T47542	Spot 3 protein and
990	79.5	5.1	361	2	JH0417	cell adhesion mole	1063	79	5.1	1096	2	T38470	probable calcium-t
991	79.5	5.1	362	2	I56130	HLA-B*5401 - human	1064	79	5.1	1609	2	S25345	probable membrane
992	79.5	5.1	362	2	I84486	transmembrane glyco	1065	79	5.1	1854	2	S36859	c1pa protein (EC 3.4
993	79.5	5.1	362	2	I62042	MHC HLA-B cell sur	1066	79	5.1	1902	1	B44658	Ig heavy chain V r
994	79.5	5.1	362	2	I37120	MHC class I histoc	1067	78.5	5.1	109	2	PL0233	Ig heavy chain V r
995	79.5	5.1	362	2	B30345	MHC class I histoc	1068	78.5	5.1	114	2	S22554	Ig heavy chain V r
996	79.5	5.1	362	2	A45834	MHC class I histoc	1069	78.5	5.1	123	2	PH1403	Ig heavy chain V6
997	79.5	5.1	362	2	I61907	MHC class I histoc	1070	78.5	5.1	125	2	S24703	Ig heavy chain pre
998	79.5	5.1	362	2	I37515	MHC class I histoc	1071	78.5	5.1	136	2	S04576	T-cell receptor de
999	79.5	5.1	362	2	C35997	MHC class I histoc	1072	78.5	5.1	139	2	S36325	H-2 class II histo
1000	79.5	5.1	362	2	I81233	lymphocyte antigen	1073	78.5	5.1	182	2	C37410	HLA-DR beta-chain
1001	79.5	5.1	362	2	I72755	HLA-B*5602 - human	1074	78.5	5.1	220	2	I68710	MHC RLA - rabbit (
1002	79.5	5.1	362	2	G01230	MHC class I histoc	1075	78.5	5.1	236	2	I46860	probable VAMP-asso
1003	79.5	5.1	362	2	I37532	MHC class I histoc	1076	78.5	5.1	239	2	H84886	myelin P0 protein
1004	79.5	5.1	362	2	I59633	MHC HLA-B transmem	1077	78.5	5.1	248	1	JH0252	MHC class II histo
1005	79.5	5.1	362	2	I61904	MHC class I histoc	1078	78.5	5.1	264	2	I48422	carcinoembryonic a
1006	79.5	5.1	362	2	I72753	HLA-B*5502 - human	1079	78.5	5.1	265	2	S69335	cell surface glyco
1007	79.5	5.1	362	2	I59654	major histocompati	1080	78.5	5.1	266	2	I67726	transcription fact
1008	79.5	5.1	362	2	I72754	HLA-B*5601 - human	1081	78.5	5.1	326	2	A45452	myristylated alant
1009	79.5	5.1	362	2	I62045	gene HLA-B-1517 pr	1082	78.5	5.1	335	2	S08341	class I histocompa
1010	79.5	5.1	362	2	I61863	MHC HLA-B*46 - hum	1083	78.5	5.1	354	2	I59308	class I histocompa
1011	79.5	5.1	362	2	S77956	MHC class I histoc	1084	78.5	5.1	354	2	I80166	class I histocompa
1012	79.5	5.1	362	2	I37519	MHC class I histoc	1085	78.5	5.1	354	2	I80167	class I histocompa
1013	79.5	5.1	362	2	I54457	MHC class I lympho	1086	78.5	5.1	354	2	I80168	MHC class I histoc
1014	79.5	5.1	362	2	I72752	HLA-B*5501 - human	1087	78.5	5.1	359	1	HLH012	MHC class I histoc
1015	79.5	5.1	362	2	I56133	MHC class I protei	1088	78.5	5.1	362	2	I68724	lymphocyte adhesio
1016	79.5	5.1	362	2	I84490	lymphocyte antigen	1089	78.5	5.1	362	2	A30901	secretory protein
1017	79.5	5.1	362	2	I54298	gene HLA-B protein	1090	78.5	5.1	399	2	S27879	interleukin-11 rec
1018	79.5	5.1	362	2	A30345	MHC class I histoc	1091	78.5	5.1	432	2	I48343	Ig mu chain C regi
1019	79.5	5.1	362	2	A45880	MHC class I histoc	1092	78.5	5.1	450	1	MHDG	Ig mu chain C regi
1020	79.5	5.1	362	2	I62043	MHC HLA-B cell sur	1093	78.5	5.1	453	2	S37768	mucin 5AC (clone J
1021	79.5	5.1	362	2	I37501	MHC class I histoc	1094	78.5	5.1	477	2	S53362	paired box transcr
1022	79.5	5.1	362	2	I62041	MHC HLA-B cell sur	1095	78.5	5.1	479	1	S15031	hypothetical prote
1023	79.5	5.1	362	2	I62044	MHC class I histoc	1096	78.5	5.1	518	2	T49778	hypothetical prote
1024	79.5	5.1	362	2	I61860	MHC HLA-B18 chain	1097	78.5	5.1	556	2	T16143	interleukin-1 rece
1025	79.5	5.1	362	2	I61789	class I histocompa	1098	78.5	5.1	576	2	A32604	Fos-related antige
1026	79.5	5.1	362	2	S24435	class I histocompa	1099	78.5	5.1	595	2	A35847	hypothetical prote
1027	79.5	5.1	362	2	S24434	class I histocompa	1100	78.5	5.1	712	2	T13617	hypothetical prote
1028	79.5	5.1	363	2	H97455	UDP-N-acetylglucos	1101	78.5	5.1	719	2	S44237	trypanastigote sur
1029	79.5	5.1	417	2	F82020	C4-dicarboxylate t	1102	78.5	5.1	740	2	G95153	neuraminidase, pro
1030	79.5	5.1	428	2	S47749	uptake of C4-dicar	1103	78.5	5.1	1378	1	I48751	protein-tyrosine k
1031	79.5	5.1	428	2	A86026	uptake of C4-dicar	1104	78.5	5.1	1539	2	S65775	homeotic protein H
1032	79.5	5.1	428	2	H91179	serine-rich protei	1105	78.5	5.1	1821	2	AG2335	hypothetical prote
1033	79.5	5.1	534	2	T39903	hypothetical protei	1106	78.5	5.1	1965	2	S25174	Ig heavy chain V r
1034	79.5	5.1	547	2	S61032	killer cell inhibi	1107	78	5.1	118	2	S04577	Ig kappa chain pre
1035	79.5	5.1	635	2	UC5886	protein F20B24.6 (1108	78	5.1	127	2	PH1288	Ig heavy chain pre
1036	79.5	5.1	715	2	G86239	S-receptor kinase	1109	78	5.1	133	2	S54234	Ig mu heavy chain
1037	79.5	5.1	824	1	S50767	macrophage colony-	1110	78	5.1	137	2	IU0284	Fc gamma (IgG) rec
1038	79.5	5.1	972	1	TVHUMD	cartilage intermed	1111	78	5.1	233	1	J50976	HLA DR-beta-III -
1039	79.5	5.1	1184	2	T09484	hypothetical prote	1112	78	5.1	239	2	I71904	HLA DR-beta-I - hu
1040	79.5	5.1	2167	2	T34395	probable invasiv	1113	78	5.1	252	2	JC2388	probable integral
1041	79.5	5.1	3013	2	AB0480	large repetitive p	1114	78	5.1	253	2	A71624	Ig alpha chain C r
1042	79.5	5.1	3624	2	AD0835	carcinoembryonic a	1115	78	5.1	299	1	AHRB	Ig alpha chain C r
1043	79	5.1	85	2	S08109	Ig heavy chain V r	1116	78	5.1	338	2	S09276	Ig heavy chain V6
1044	79	5.1	98	2	S26914	T-cell receptor be	1117	78	5.1	400	1	A39822	Ig heavy chain, be
1045	79	5.1	111	2	E27552	Ig mu heavy chain	1118	78	5.1	402	2	S20002	Ig heavy chain -
1046	79	5.1	140	2	S54248	Ig heavy chain V r	1119	78	5.1	433	2	S31436	interleukin-6 rece
1047	79	5.1	140	2	PH1462	Ig heavy chain V r	1120	78	5.1	440	2	IL0144	interleukin-6 rece
1048	79	5.1	154	2	S23044	class II histocomp	1121	78	5.1	460	2	JL0145	flagellar basal-do
1049	79	5.1	244	2	S23982	prgk protein - Sal	1122	78	5.1	550	2	A11163	vacuolar sorting r
1050	79	5.1	252	2	S69786	MHC class II histo	1123	78	5.1	624	2	T00044	
1051	79	5.1	253	2	S15684		1124	78	5.1	624	2		

1125	78	5.1	678	2	T39151	translation initia	1198	77	5.0	392	2	G70146	methionine adenosy
1126	78	5.1	744	2	A4353	aectles sialoglyco	1199	77	5.0	405	1	GMSEW	Ig gamma-2b chain
1127	78	5.1	857	2	S44883	ZC262.3 protein -	1200	77	5.0	412	2	D72364	conserved hypochet
1128	78	5.1	875	2	H90371	protease limprot	1201	77	5.0	468	1	A41242	interleukin-6 rece
1129	78	5.1	902	2	T47966	hypothetical prote	1202	77	5.0	490	2	F67443	conserved hypochet
1130	78	5.1	912	2	D72644	hypothetical prote	1203	77	5.0	497	2	T14433	reproductive mexis
1131	78	5.1	1081	2	T31094	surface antigen B6	1204	77	5.0	499	1	B64069	fructose phosphor
1132	78	5.1	1123	2	C96622	probable ATPase F2	1205	77	5.0	516	2	T49422	RAD57 related prot
1133	78	5.1	1188	2	UC4889	phosphatidylinosit	1206	77	5.0	569	2	A46462	T cell activation
1134	78	5.1	1219	2	T14578	nucleoporin Nup153	1207	77	5.0	595	2	A10042	thiol,disulfide in
1135	78	5.1	1287	2	T21312	hypothetical prote	1208	77	5.0	613	2	T27528	hypothetical prote
1136	77.5	5.0	103	1	K5RB	Ig kappa-B5 chain	1209	77	5.0	664	2	JC7990	acetylcholinestera
1137	77.5	5.0	119	2	S45714	Ig heavy chain V r	1210	77	5.0	700	2	C68296	hypothetical prote
1138	77.5	5.0	134	2	A45893	T-cell receptor al	1211	77	5.0	726	2	T33998	hypothetical prote
1139	77.5	5.0	149	2	B40463	integrin alpha-6 c	1212	77	5.0	772	2	T48747	hemaphorin D - mu
1140	77.5	5.0	150	2	PN0444	Ig heavy chain V r	1213	77	5.0	803	2	T04190	subtilisin-like pr
1141	77.5	5.0	215	2	S61337	proteasome endopep	1214	77	5.0	825	2	T29634	hypothetical prote
1142	77.5	5.0	219	1	A29128	myelin P0 protein	1215	77	5.0	829	2	T46536	Kap-cadherin - rab
1143	77.5	5.0	232	1	HLMSE2	H-2 class II histo	1216	77	5.0	986	1	A29646	invasin - Yersinia
1144	77.5	5.0	237	2	A21200	H-2 class II histo	1217	77	5.0	991	2	T70843	receptor protein-t
1145	77.5	5.0	241	2	H96691	hypothetical prote	1218	77	5.0	1087	1	S41797	cellulose 1,4-beta
1146	77.5	5.0	249	2	S69340	Ig heavy chain VH	1219	77	5.0	1802	2	S69703	HK1 protein precu
1147	77.5	5.0	250	2	A28564	lymphocyte functio	1220	77	5.0	3034	2	T14119	seven-pass transme
1148	77.5	5.0	250	2	S19518	hypothetical prote	1221	76.5	5.0	115	2	S03482	Ig heavy chain V-D
1149	77.5	5.0	264	2	T26976	hypothetical prote	1222	76.5	5.0	139	2	S54231	Ig mu heavy chain
1150	77.5	5.0	266	2	B28031	MHC class II histo	1223	76.5	5.0	144	2	S54228	Ig mu heavy chain
1151	77.5	5.0	309	2	T34071	hypothetical prote	1224	76.5	5.0	220	2	A25925	class II histocomp
1152	77.5	5.0	302	2	T15747	hypothetical prote	1225	76.5	5.0	224	2	I72443	CMRF-35 antigen -
1153	77.5	5.0	348	2	S09270	Ig alpha chain C r	1226	76.5	5.0	262	2	T01562	hypothetical prote
1154	77.5	5.0	350	2	I54308	MHC HLA B71 - huma	1227	76.5	5.0	315	2	S58689	hypothetical prote
1155	77.5	5.0	382	2	T46519	probable glycosyl	1228	76.5	5.0	317	2	T37442	Ebv gp42,ps/hr pro
1156	77.5	5.0	391	1	MHRUBT	Ig mu heavy chain	1229	76.5	5.0	353	2	D87539	hypothetical prote
1157	77.5	5.0	430	2	T28143	leptasin I homolog,	1230	76.5	5.0	357	2	S11133	class I histocompa
1158	77.5	5.0	462	2	AH1184	wall associated pr	1231	76.5	5.0	362	2	C40730	MHC HLA-B*44.2 cha
1159	77.5	5.0	465	2	A44498	radial spoke prote	1232	76.5	5.0	362	2	I61861	class I histocompa
1160	77.5	5.0	477	2	H75026	oligopeptide abc t	1233	76.5	5.0	362	2	S25415	class I histocompa
1161	77.5	5.0	498	2	S11246	LAC-3 protein prec	1234	76.5	5.0	365	2	S77963	MHC class I histo
1162	77.5	5.0	555	2	UQ1526	interleukin-1 rece	1235	76.5	5.0	365	2	T54416	HLA-A*24 protein -
1163	77.5	5.0	590	2	B86440	probable protein k	1236	76.5	5.0	365	2	I54493	MHC class I histo
1164	77.5	5.0	634	2	C96541	10-formyletrahydr	1237	76.5	5.0	370	2	H84351	hypothetical prote
1165	77.5	5.0	679	2	S06000	penicillin-binding	1238	76.5	5.0	418	2	S66073	hypothetical prote
1166	77.5	5.0	966	2	H97717	probable PPE prote	1239	76.5	5.0	419	2	S56073	oposue-2 protein -
1167	77.5	5.0	987	2	E70808	hypothetical prote	1240	76.5	5.0	448	2	A38445	EV12B protein prec
1168	77.5	5.0	1027	2	D85757	probable efflux pu	1241	76.5	5.0	456	2	T38221	hypothetical serin
1169	77.5	5.0	1027	2	H90861	probable multidrug	1242	76.5	5.0	510	2	S45571	nuclear factor I-C
1170	77.5	5.0	1073	2	B36429	integrin alpha-6 c	1243	76.5	5.0	549	2	F05485	Ig heavy chain pre
1171	77.5	5.0	1353	2	T00249	incl protein - ink	1244	76.5	5.0	574	2	F75356	serine/threonine p
1172	77.5	5.0	1441	2	A86685	prophage pil prote	1245	76.5	5.0	621	2	T38467	low density lipopr
1173	77.5	5.0	1452	1	S17669	protein-tyrosine-p	1246	76.5	5.0	671	2	C63934	methyl-accepting c
1174	77.5	5.0	1452	1	S17670	probable peptidogl	1247	76.5	5.0	709	2	S38883	polynribonucleotide
1175	77.5	5.0	2044	2	AB1180	polycystic kidney	1248	76.5	5.0	771	2	S25814	hypothetical prote
1176	77.5	5.0	4302	2	A38971	T-cell receptor al	1249	76.5	5.0	839	2	T04859	extensin homolog F
1177	77	5.0	118	2	B32536	T-cell receptor al	1250	76.5	5.0	849	2	T04242	abdominal segment
1178	77	5.0	130	2	S04542	Ig kappa chain pre	1251	76.5	5.0	938	2	AR1772	internalin-like pr
1179	77	5.0	134	2	PC1214	Ig heavy chain V r	1252	76.5	5.0	1041	2	S55862	probable membrane
1180	77	5.0	135	2	PH1492	Ig heavy chain pre	1253	76.5	5.0	1248	2	C69874	autolyisin [impor
1181	77	5.0	137	2	PH1227	Ig heavy chain pre	1254	76.5	5.0	2397	1	A55535	versalin precursor
1182	77	5.0	140	1	HVMSG7	Ig heavy chain V r	1255	76.5	5.0	2809	2	T30213	G-cadherin - sea u
1183	77	5.0	140	2	A36194	Ig heavy chain V r	1256	76	4.9	118	2	PL0084	Ig heavy chain V r
1184	77	5.0	140	2	PH1483	Ig heavy chain V r	1257	76	4.9	120	2	PS0089	Ig heavy chain V r
1185	77	5.0	144	2	PH1284	Ig heavy chain pre	1258	76	4.9	133	2	T45927	membrane-bound im
1186	77	5.0	216	2	S69130	Ig lambda chain (D	1259	76	4.9	138	2	S21810	Ig heavy chain V r
1187	77	5.0	219	2	PC4203	Ig kappa chain (mo	1260	76	4.9	139	2	S31678	Ig heavy chain V r
1188	77	5.0	229	2	A48381	MHC class II histo	1261	76	4.9	140	2	PH1498	Ig heavy chain V r
1189	77	5.0	259	2	A98049	conserved hypochet	1262	76	4.9	141	2	I57007	pregnancy-specific
1190	77	5.0	259	2	F95181	MHC PDb-glycoprote	1263	76	4.9	142	2	S54241	Ig mu heavy chain
1191	77	5.0	350	2	I46608	MHC class II antige	1264	76	4.9	192	2	T39464	CDB antigen - huma
1192	77	5.0	352	2	I51541	class I histocompa	1265	76	4.9	223	2	I46696	MHC class II prote
1193	77	5.0	353	2	B53250	major histocompat	1266	76	4.9	233	2	I55654	Ig kappa chain pre
1194	77	5.0	355	2	I51309	class I histocompa	1267	76	4.9	234	2	S01320	MHC H2-IE-beta cel
1195	77	5.0	357	2	S09269	Ig alpha chain C r	1268	76	4.9	238	2	I71907	I-E(b-beta) protei
1196	77	5.0	357	2	S09269	Ig alpha chain C r	1269	76	4.9	241	2	I48657	
1197	77	5.0	357	2	S09265	Ig alpha chain C r	1270	76	4.9	264	1	HLMSE1	H-2 class II histo

1271	76	4.9	264	1	HLMSEB		1344	75.5	4.9	2329	2	S44625	C50C3.6 protein -
1272	76	4.9	264	2	A30529	H-2 class II histo	1345	75	4.9	115	2	S13726	Ig lambda chain v r
1273	75	4.9	268	2	C87579	TonB-dependent rec	1346	75	4.9	121	2	S31602	Ig heavy chain v r
1274	76	4.9	269	2	S57494	T-cell receptor al	1347	75	4.9	122	2	S11740	Ig heavy chain pre
1275	76	4.9	354	2	T38306	guanine nucleotide	1348	75	4.9	132	2	S26882	Ig kappa chain v r
1276	76	4.9	362	2	A45897	MHC class I histoc	1349	75	4.9	135	2	PH1493	Ig heavy chain v r
1277	76	4.9	363	2	S07113	Class I histocompa	1350	75	4.9	136	2	B47159	Ig heavy chain v r
1278	76	4.9	365	2	T38720	hfeRn - human	1351	75	4.9	137	2	B34903	Ig heavy chain pre
1279	76	4.9	374	1	A39878	FC gamma (IgG) rec	1352	75	4.9	140	2	PH1484	Ig heavy chain v r
1280	76	4.9	397	2	B27496	proteinase inhibic	1353	75	4.9	288	2	S29690	Ig heavy chain v r
1281	76	4.9	444	2	PC4456	monoclonal antibod	1354	75	4.9	301	2	A60548	synaptophysin - Pa
1282	76	4.9	449	1	B43698	paired box transcr	1355	75	4.9	321	2	B81668	conserved hypochet
1283	76	4.9	474	2	S15590	Ig heavy chain - h	1356	75	4.9	342	2	S39601	Class I histocompa
1284	76	4.9	475	2	S01321	Ig gamma-2b chain	1357	75	4.9	344	1	AHMS	Ig alpha chain C r
1285	76	4.9	500	1	ITTHUC1	complement C1 inh	1358	75	4.9	354	2	A46393	GTP-binding protei
1286	76	4.9	550	2	A11522	flagellar basal-bo	1359	75	4.9	355	2	I80171	class I histocompa
1287	76	4.9	651	2	A96591	NPx1-related prote	1360	75	4.9	358	2	F70577	probable lipoprote
1288	76	4.9	669	2	I38029	matrix metalloprot	1361	75	4.9	363	2	S03537	Class I histocompa
1289	76	4.9	711	2	AD0901	polynucleotide pho	1362	75	4.9	372	2	C39371	Ig V-region-like B
1290	76	4.9	720	2	G97229	pullulanase (limpor	1363	75	4.9	373	2	S43455	hypothetical prote
1291	76	4.9	753	2	T24869	hypothetical prote	1364	75	4.9	387	2	I50703	transcription fact
1292	76	4.9	798	2	H87271	hypothetical prote	1365	75	4.9	391	2	T09058	butyrophilin homol
1293	76	4.9	841	2	UC5894	tonB-dependent rec	1366	75	4.9	406	1	S48820	serine-type D-Ala-
1294	76	4.9	846	2	C82135	killer cell inhibi	1367	75	4.9	429	2	G97025	probable membrane
1295	76	4.9	906	2	G90281	chitinase Vc1952 l	1368	75	4.9	438	1	HVRKC2	Ig mu chain C regl
1296	76	4.9	1072	2	S76888	conserved hypochet	1369	75	4.9	451	2	T49011	hypothetical prote
1297	76	4.9	1175	2	T46124	hypothetical prote	1370	75	4.9	462	1	A37986	interleukin-6 rece
1298	75.5	4.9	115	2	A25924	hypothetical prote	1371	75	4.9	463	2	T15876	hypothetical prote
1299	75.5	4.9	118	2	S37201	Ig kappa chain pre	1372	75	4.9	474	1	G2MS11	Ig gamma-2b chain
1300	75.5	4.9	131	1	KVSM6	Ig heavy chain v r	1373	75	4.9	532	1	A29849	intercellular adhe
1301	75.5	4.9	138	2	I46634	Ig kappa chain pre	1374	75	4.9	643	2	T21296	hypothetical prote
1302	75.5	4.9	153	2	S31700	rearranged T-cell	1375	75	4.9	645	2	E96631	probable receptor
1303	75.5	4.9	185	2	S37479	Ig heavy chain v r	1376	75	4.9	695	2	T39954	probable gpase ac
1304	75.5	4.9	215	2	JB0244	T-cell receptor al	1377	75	4.9	724	2	D96349	secreted protein c
1305	75.5	4.9	261	2	S17889	Ig kappa chain NIG	1378	75	4.9	725	2	A41258	a-agglutinin core
1306	75.5	4.9	269	2	T42919	Class II histocomp	1379	75	4.9	825	2	T27852	hypothetical prote
1307	75.5	4.9	322	2	PS0019	protein t10 - atel	1380	75	4.9	860	2	JC4566	chitinase (EC 3.2.
1308	75.5	4.9	333	2	AF0407	Ig gamma-2a chain	1381	75	4.9	881	2	S56032	probable membrane
1309	75.5	4.9	343	2	S25644	lipoprotein (limpor	1382	75	4.9	1104	2	S59310	probable membrane
1310	75.5	4.9	345	1	HLCHB4	Ig mu chain C regl	1383	75	4.9	1386	2	AC1533	surface protein (L
1311	75.5	4.9	349	2	T42965	MHC class I histoc	1384	75	4.9	1472	2	B54774	ATP binding casaset
1312	75.5	4.9	354	2	S18197	glycoprotein - ate	1385	75	4.9	1474	2	D88550	protein ZC84.6 (Im
1313	75.5	4.9	355	2	T28152	Class I histocompa	1386	75	4.9	3973	2	B71612	hypothetical prote
1314	75.5	4.9	357	2	I36966	MHC class I histoc	1387	75	4.9	95	2	S25177	Ig kappa chain v r
1315	75.5	4.9	362	2	JH0538	Class I histocomp	1388	74.5	4.8	106	2	PH1002	Ig heavy chain v r
1316	75.5	4.9	408	2	S42423	Class I histocomp	1389	74.5	4.8	112	2	C44151	Ig lambda chain v r
1317	75.5	4.9	411	2	A11161	opague 2 protein -	1390	74.5	4.8	112	2	S43146	Ig upslion chain -
1318	75.5	4.9	417	2	A11520	flagellar hook pro	1391	74.5	4.8	123	2	A36006	Ig heavy chain v r
1319	75.5	4.9	417	2	A81248	flagellar hook pro	1392	74.5	4.8	142	2	S31671	Ig heavy chain v r
1320	75.5	4.9	457	2	A27449	UDP-N-acetylglucos	1393	74.5	4.8	144	2	S11244	Ig gamma-2a chain
1321	75.5	4.9	463	2	C86341	T-cell surface gly	1394	74.5	4.8	219	2	S52028	Ig kappa chain - m
1322	75.5	4.9	472	2	T24316	PDH16.15 protein-	1395	74.5	4.8	248	2	B45831	MHC class I histoc
1323	75.5	4.9	475	2	S47861	hypothetical prote	1396	74.5	4.8	254	2	B31790	MHC class I histoc
1324	75.5	4.9	477	2	T46917	mei-1 protein - Ca	1397	74.5	4.8	261	2	B31790	Ig heavy chain v r
1325	75.5	4.9	495	2	S76967	hypothetical prote	1398	74.5	4.8	264	2	B30582	FC gamma (IgG) rec
1326	75.5	4.9	502	2	A48679	hypothetical prote	1399	74.5	4.8	276	2	S20690	MHC class II histo
1327	75.5	4.9	555	2	T21028	differentiated ker	1400	74.5	4.8	317	2	D42526	31.6k hypochetical
1328	75.5	4.9	760	2	F86387	hypothetical prote	1401	74.5	4.8	331	2	A54295	BSR protein - vacc
1329	75.5	4.9	768	2	F84237	probable Pto Kinase	1402	74.5	4.8	331	2	S53501	interferon alpha/b
1330	75.5	4.9	784	2	T48897	Hcra transducer [i	1403	74.5	4.8	339	2	S09264	interferon recepto
1331	75.5	4.9	784	2	T20074	transducer protein	1404	74.5	4.8	341	2	T45839	Ig alpha chain C r
1332	75.5	4.9	786	2	T16509	hypothetical prote	1405	74.5	4.8	342	2	A46529	probable cysteine
1333	75.5	4.9	796	2	T21460	hypothetical prote	1406	74.5	4.8	344	2	B28967	Ig gamma chain (5.
1334	75.5	4.9	829	2	D71485	probable adenylyate	1407	74.5	4.8	360	2	A27638	T-cell surface gly
1335	75.5	4.9	843	2	S57653	brevican precursor	1408	74.5	4.8	362	2	T18421	MHC class I histoc
1336	75.5	4.9	947	2	T23107	hypochetical prote	1409	74.5	4.8	371	2	A53908	gene HLA B-1519 pr
1337	75.5	4.9	1019	2	T13039	tyrosine kinase re	1410	74.5	4.8	383	2	T21946	brevican precursor
1338	75.5	4.9	1045	2	S60571	integrin alpha v c	1411	74.5	4.8	419	2	S14508	hypochetical prote
1339	75.5	4.9	1118	2	H97298	subtilisin like pr	1412	74.5	4.8	445	2	T21744	asparaginase-rich pr
1340	75.5	4.9	1125	1	S57846	protein-tyrosine k	1413	74.5	4.8	473	2	B84853	hypochetical prote
1341	75.5	4.9	1152	1	AC1347	probable peptidogl	1414	74.5	4.8	515	2	I139073	interferon alpha-b
1342	75.5	4.9	1433	1	A36734	baclillopeptidase F	1415	74.5	4.8	528	2	PC4025	intercellular adhe
1343	75.5	4.9	1530	2	I45944	neurexin I-alpha -	1416	74.5	4.8	552	1	S35703	colony-stimulating

1417	74.5	4.8	552	1	A31401	macrophage colony-
1418	74.5	4.8	590	2	A44068	cell pattern forma
1419	74.5	4.8	643	2	AC2199	phosphorylpyruvat
1420	74.5	4.8	710	2	S63598	cyclomaldextrin
1421	74.5	4.8	761	1	IJBODE	desmocollextin
1422	74.5	4.8	806	2	E59424	hypothetical prote
1423	74.5	4.8	819	2	MMECOF	outer membrane un
1424	74.5	4.8	832	1	IJBODF	desmocolin 1b pre
1425	74.5	4.8	869	2	T44440	chitinase (EC 3.2.
1426	74.5	4.8	883	2	S49126	brevian precursor
1427	74.5	4.8	912	2	A54423	brevian precursor
1428	74.5	4.8	952	2	T32836	hypothetical prote
1429	74.5	4.8	988	2	I50611	protein-tyrosine k
1430	74.5	4.8	992	2	A39931	protein-tyrosine k
1431	74.5	4.8	1000	2	S18827	Flt3 protein - mou
1432	74.5	4.8	1116	2	S63397	probable membrane
1433	74.5	4.8	1138	1	S24065	protein-tyrosine k
1434	74.5	4.8	1141	1	GNVUSV	M polyprotein prec
1435	74.5	4.8	1582	2	AC1153	adhesin homolog 1m
1436	74.5	4.8	1601	2	AB1730	hypothetical prote
1437	74.5	4.8	3029	2	S76109	hypothetical prote
1438	74	4.8	115	2	PL0238	Ig heavy chain v r
1439	74	4.8	117	2	PL0237	Ig heavy chain v r
1440	74	4.8	117	2	PL0235	Ig heavy chain v r
1441	74	4.8	118	2	PL0231	Ig heavy chain v r
1442	74	4.8	119	2	PH1505	Ig heavy chain v r
1443	74	4.8	120	2	G28195	Ig heavy chain v r
1444	74	4.8	123	2	S24693	Ig heavy chain v r
1445	74	4.8	133	2	S34010	Ig heavy chain v r
1446	74	4.8	135	2	I46643	rearranged T-cell
1447	74	4.8	135	2	PL0100	Ig heavy chain pre
1448	74	4.8	144	2	S54244	Ig mu heavy chain
1449	74	4.8	228	2	S03050	Ig heavy chain (cl
1450	74	4.8	229	2	I45936	MHC lymphocyte ant
1451	74	4.8	237	2	B28043	MHC class II histo
1452	74	4.8	246	2	I50094	MHC class II beta
1453	74	4.8	248	2	S35076	class II histocomp
1454	74	4.8	255	2	I47092	MHC OVAR-DQ-ALPHA
1455	74	4.8	261	2	A55242	MHC class II histo
1456	74	4.8	277	2	AB1390	hypothetical cell
1457	74	4.8	329	1	A48754	B7-2 antigen - hum
1458	74	4.8	332	2	T45770	hypothetical prote
1459	74	4.8	347	2	S09274	Ig alpha chain C r
1460	74	4.8	365	2	JH0534	class I histocomp
1461	74	4.8	365	2	I84432	MHC class I protei
1462	74	4.8	386	2	Ti3940	hypothetical prote
1463	74	4.8	396	2	T01049	hypothetical prote
1464	74	4.8	401	2	A40364	probable H1YD faml
1465	74	4.8	404	2	AA4833	lactocobin (EC 3.4
1466	74	4.8	409	2	AB3624	acriflavin resista
1467	74	4.8	463	2	T14884	hypothetical prote
1468	74	4.8	472	2	G87068	pyruvate kinase (i
1469	74	4.8	492	2	B86911	probable penicilli
1470	74	4.8	520	2	S62521	hypothetical prote
1471	74	4.8	521	2	S54266	glycoprotein gc -
1472	74	4.8	547	1	S28904	intercellular adhe
1473	74	4.8	571	2	T08830	hypothetical prote
1474	74	4.8	609	2	J00703	glycogen(starch) s
1475	74	4.8	609	2	S11481	glycogen(starch) s
1476	74	4.8	619	2	A43361	Ets-related transc
1477	74	4.8	726	2	T40790	probable permease
1478	74	4.8	734	2	H65106	polynucleotide
1479	74	4.8	734	2	H85979	polynucleotide pho
1480	74	4.8	734	2	E91134	polynucleotide pho
1481	74	4.8	737	2	T46101	ABC transporter-11
1482	74	4.8	753	2	G02173	semaphorin 111 fam
1483	74	4.8	791	2	T16031	hypothetical prote
1484	74	4.8	888	2	S47489	receptor tyrosine
1485	74	4.8	1020	2	H96793	unknown protein F1
1486	74	4.8	1036	2	A29832	HPT layer surface
1487	74	4.8	1072	2	T00041	BH-protocadherin P
1488	74	4.8	1141	2	E89824	hypothetical prote
1489	74	4.8	1200	2	T00042	BH-Protocadherin P
1490	74	4.8	1251	2	T21389	hypothetical prote
1491	74	4.8	1353	2	T19691	hypothetical prote
1492	74	4.8	1417	2	H90670	probable invasiv
1493	74	4.8	1417	2	D85521	probable adhesin
1494	74	4.8	1417	2	C97012	probably cellulose
1495	74	4.8	1493	2	A32534	lactocoeptin (EC 3.4
1496	74	4.8	2508	2	S61441	surface-associated
1497	74	4.8	3705	2	AD0123	surface autotrans
1498	74	4.8	3716	2	E70969	probable PPE prote
1499	74	4.8	4436	2	E71086	hypothetical prote
1500	73.5	4.8	116	1	HVMS1B	Ig heavy chain pre
ALIGNMENTS						
RESULT 1						
S56749						
Junctional adhesion molecule precursor - human						
N:Alternate names: F11 platelet antigen; platelet adhesion molecule PM-1; platelet F11						
C:Species: Homo sapiens (man)						
C:Date: 27-Oct-1995 #sequence #revision 01-Feb-2002 #text_change 09-Jul-2004						
C:Accession: A59406; S56749						
R:Ozaki, H.; Ishii, K.; Horitsuichi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K						
J. Immunol. 163, 553-557, 1999						
A:Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi						
A:Reference number: A59406; MUID:99323940; PMID:10395639						
A:Accession: A59406						
A:Status: preliminary						
A:Molecule type: DNA						
A:Residues: 1-299 <OZA>						
A:Cross-references: UNIPROT:Q9Y624; UNIPARC:UPI0000000DC1; GB:AAD42050; NID:95336797; PI						
R:Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.						
Biochem. J. 310, 155-162, 1995						
A:Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a						
A:Reference number: S56749; MUID:95374438; PMID:7646439						
A:Accession: S56749						
A:Molecule type: protein						
A:Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDTIYLNXY','LT',206,'X'						
A:Cross-references: UNIPARC:UPI00001468C; UNIPARC:UPI00001468C; UNIPARC:UPI00001468D;						
A>Note: the order of the peptides other than the amino terminus was not determined						
C:Genetics:						
A:Gene: JAM						
C:Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane						
F:1-25/Domain: signal sequence #status predicted <Sig>						
F:26-299/Product: junctional adhesion molecule #status predicted <Mat>						
Query Match 100.0%; Score 1544; DB 2; Length 299;						
Best Local Similarity 100.0%; Pred. No. 3.3e-105;						
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MGTAAQVERKLLCLFIATILLCSIALGSGTVVHSSPEPRVIRPENNPVKLSGAYGFSFSPRV	60			
DB	1	MGTAAQVERKLLCLFIATILLCSIALGSGTVVHSSPEPRVIRPENNPVKLSGAYGFSFSPRV	60			
QY	61	EMKPDGDITRLVCNNKKTASIEDRYTFLPTGITFSVYREDTGTTCVNSEGGSNG	120			
DB	61	EMKPDGDITRLVCNNKKTASIEDRYTFLPTGITFSVYREDTGTTCVNSEGGSNG	120			
QY	121	EVKKVLIVLPSPKPTVINPSSATIGNRAVLITCSBODGSPSESYTFPKDGIWPTPKST	180			
DB	121	EVKKVLIVLPSPKPTVINPSSATIGNRAVLITCSBODGSPSESYTFPKDGIWPTPKST	180			
QY	181	RAFSNSSYVNPPTTGEIVPDPPLASDGTGEVSCANRGYGTGPMTSMNAVREAVRRNNGVIV	240			
DB	181	RAFSNSSYVNPPTTGEIVPDPPLASDGTGEVSCANRGYGTGPMTSMNAVREAVRRNNGVIV	240			
QY	241	AAVAVTLLILGILVFGIWFPAYSRSGHFDRTKGTSSKVVITYSPSASSEGFKOTSSFLV	299			
DB	241	AAVAVTLLILGILVFGIWFPAYSRSGHFDRTKGTSSKVVITYSPSASSEGFKOTSSFLV	299			
RESULT 2						

Query Match 11.8%; Score 181.5; DB 2; Length 866;
Best Local Similarity 29.3%; Pred. No. 1.7e-05;

Matches 76; Conservative 32; Mismatches 84; Indels 67; Gaps 16;

OY 22 CSLALGSV-TTHSSEPRRIENNPN-----VKLSC-AVGFSPRMEKFFDDGDT 69
||| ||| : | : : : : :
Db 512 CSMALPVTLNVAHPDRDKVLKVSASEIRAGORVLLQCDFAENPAAVFPEFK----- 565
OY 70 TRLVCCNNKIITASYEDRYTFPTGITFEKSVTREDTGTYTCMVSEGGNSYGEEVAK---L 126
566 -----KNGSLV--DEGRY-----LSFGSVSPEDSGANNCMNV----NSIGETLSQAMNL 608
Db 127 ILYVPSPSKFTYN-IPSATI-GNRAVLTCSDQSPP-SETTWKDGIIWFPNKSTRAF 183
OY 609 QVLVAFRRLRSIIPGDHVEGKKATLSC-ESDANNPISQYLW-----F 651
184 SNSSYVNLPPTGEIVFDPLASDGTGEYSCEARNAYGT---PMTSNARMAVERNAVGI 239
Db 652 DSSGODLHSQQKRLERLELEVQHGTSTRCKTNGIGTESPST--LTVIYSPETTICKR 708
OY 240 VAAVLVTLLLGLILVFGLM 258
Db 709 VALGLG--FCLLTIFILAIM 725

RESULT 6

JC2457

Vascular cell adhesion protein - pig

C:Species: Sus scrofa domestica (domestic pig)
C>Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: JC2457
C:Release: Y.T.M.; Haskard, D.O.; Robinson, M.K.
Biochem. Biophys. Res. Commun. 201, 805-812, 1994
A>Title: Cloning and expression kinetics of porcine vascular cell adhesion molecule.
A:Reference number: JC2457; MUID:94271236; PMID:7516159
A:Accession: JC2457
A:Molecule type: mRNA
A:Residues: 1-538 <TSA>
A:CROSS-references: UNIPROT:Q28939; UNIPARC:UP1000008155; EMBL:U08351; NID:g474382; PINT:
C:Keywords: glycoprotein; transmembrane protein
F:497-517/Domain: transmembrane #status predicted <TM>
F:75,157,271,330,360/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.6%; Score 179; DB 2; Length 538;
Best Local Similarity 21.5%; Pred. No. 1.5e-05;
Matches 70; Conservative 45; Mismatches 100; Indels 110; Gaps 12;

OY 31 VHSEPEPRIENNPNVLKSCAVSGSSPRVEM-KPDGDTTRLVCYNNKITASYEDRYT 88
||| ||| : | : : : : :
Db 225 VISVNPSTSLOEGSMNMHTCTSEGPAPOISMWSKKLDND-QQLLSGN----- 271
OY 89 FLPTGITPKSVTRBDTGTYTCMVSEGGNSYG-EVKVLIIVLPPSKFTVINIPSATI- 145
272 ---ATLTIARMEDSGIYYC-----EGVNPVGTNRKEVELTVQAAPRTTISVNPSSLTE 324
OY 146 GNRAVLTCSDQSPPSEETWFK---DGIWPMNPKST----- 180
Db 325 EGSSVMNTCS-SDFGPAPKILMSKKLRDGNLEPLESENTTLTLTSTKMDSGIYVCEGINQ 383
OY 181 -----RAPSNSGY----- 188
Db 384 AGIRKEVELLIQAAPKDOLTAEPSESVEKGDTVIIISCTCGANVPRTLIIIKKALETGDT 443
OY 189 VLNPFTGELVEDPLASDGTGEYSCEARNAYGTPTMTSNARMAVERNAVGIIVAALV--- 245
444 VLKSTDGAITYIHRLADAGVYECSKNEIGLQRISTILDVGKESMDKYRSSSLAVLYC 503
246 --TLIL--LGILVFGLMAYSRGHF 266
Db 504 ASSLIIPAIGVIIYFARKANKRGY 528

RESULT 7

UH0371
B-cell adhesion protein CD22 beta splice form precursor - human

N:Alternate names: B-cell membrane protein CD22

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

CAccession: JH0371; 1561171

R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.

J. Exp. Med. 173, 137-146, 1991

A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction

A:Reference number: JH0371; MUID:91086838; PMID:1955119

A:Accession: JH0371

A:molecule type: mRNA

A:Residues: 1-847 <MIL2>

A:Cross-references: UNIPROT:060926; UNIPARC:UPI0000161B10; GB:X59350; NID:936090; PIDN:C

A:Experimental source: B lymphocyte

A:Note: the authors translated the codon AAT for residue 358 as Met

R:Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.

J. Immunol. 150, 5013-5024, 1993

A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.

A:Reference number: 1561171; MUID:93267103; PMID:8496602

A:Accession: 1561171

A>Status: translated from GB/EMBL/DBJ

A:molecule type: DNA

A:Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <MIL2>

A:Cross-references: UNIPARC:UPI000006EBA4; GB:561375; NID:9385980; PIDN:AAC18956.1; PID:

C:Genetics:

A:Gene: GDB:CD22

A:Cross-references: GDB:127545; OMIM:107266

A:Map position: 19q13.1-19q13.1

A:Intons: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3

C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>

F:346-398/Domain: immunoglobulin homology <IMM2>

F:609-661/Domain: immunoglobulin homology <IMM2>

F:688-706/Domain: transmembrane #status predicted <TRA>

F:67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)

F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 11.6%; Score 178.5; DB 2; Length 847;

Best Local Similarity 25.6%; Pred. No. 2,7e-05;

Matches 69; Conservative 42; Mismatches 100; Indels 59; Gaps 12;

29 VYVHSEPEVRIPENNPKVLSCAYSGSSPRVEMKFGQDPTRLVCYNNKITASYEDRYT 88

508 VVRKIKPKPSETHSGNSVSIQCDFSSHPKVEQPFWEK-----NGRIIL 550

89 FAPPTGTFPKSVTRREDTGTYTCWSEEGNSYGEKVV-----LIVLPSPKPTVINIPSSATI 145

551 GKESQANFQISIEDGASYSQWN-----NSIGQASAKMTLEVLVAPRLRNVSPGQDV 606

146 --GNRAVLTCSEODGSP--SEYTWFXDGIYPTNPKSTRAFNSSSYLVNPTTGEIVFDPL 202

607 MEKGSATLTC--SSDANPVPVSHYTFD-----WNQS--LPHNSQKRLRPV 649

203 SASDGEYSCEARNGV---TPMTSNAY--RMEAVERNNGVYAAVLVTLLILGLIVPGI 257

650 KYQHSQAYVCCQGNVSGKRSPLSTLVVYSPETIGRAVAGLSALILIL--ATGCL 706

258 WFAVSGHFDPTTKGTSSKKVIVSQPSARS 287

707 -----KIQRRWKRTQSQGLQENSSGQS 729

RESULT 8

T17346

hypothetical protein DKFZ58601624.1 - human (Fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

CAccession: T17346

R:Diesterhoef, A.; Labber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, September 1999

A:Molecule type: DNA
A:Residues: 1-1227 <Wtl>
A:Cross-reference: UNIPROT:O21038; UNIPARC:UPI0000077DBB; EMBL:Z68005; PDB:CAA9190.1;
A:Experimental source: clone f59f3
C:Gene: CESP:F59F3.1
A:Map position: X
A:Introns: 31/3; 58/1; 279/3; 429/2; 544/3; 638/2; 801/2; 887/1; 929/2; 1025/3; 1062/2;

Query Match 11.2%; Score 172.5; DB 2; Length 1227;
Best Local Similarity 24.0%; Pred. No. 0.0011;
Matches 65; Conservative 35; Mismatches 108; Indels 63; Gaps 9;

Qy 34 SEPEIRIENNPNVKSVCASVSGSSP-RVEMKPDQDITRLVYNNKKTASVDRITPPT 92
Db 576 SEPSKITIYEGDNVKTCTVCPPLDSDMSVSRPN-----SKSSDLSISPT 620
Qy 93 G-----ITFKSVTRDPTGTTCMVSEEGNSYGEVKVLTIVLPSPKPTVNI 139
Db 621 TTEIRIKQYSKHLINLADVTTSPTGTTCVKNEDSEKLTSIDVKAII--SKPST-- 675
Qy 140 PSSATIGNRAVLTCSEOD-----GSPPEYTWFKDGIWPTNPKSTRAFSNSYV 189
Db 676 ---TGNSNNAVIVDYDQYFEINCMGTGPPEVYQWFKDG-----NPTHGDDVDSILR 726
Qy 190 LNPFTTGELVPPLASDPTGESCERANGYGTMTSNAYRMEAVERNVGYVAALVTIL 249
Db 727 VSRAGE-----DDEEPICLATNRAGDLSIEVQVNNAPKG-SLFFYWFALLIL 776
Qy 250 LGILVFGIWPAYSRGHFDRTKKGTSSKKVIY 280
Db 777 ISIAVFLTKLRASNRLTKOKDIALMTLY 807

RESULT 12

A58532
glial cell membrane glycoprotein LIG-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: A58532
R:Stuiki, Y.; Sato, N.; Tohyama, M.; Wanaika, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A:Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in A:Reference number: A58532; MUID:96394313; PMID:8798419
A:Accession: A58532
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1091 <SUZ>
A:Cross-reference: UNIPROT:P70193; UNIPARC:UPI0000029B57; GB:D78572; NID:G1545806; PDB: F36-61/Domain: proteoglycan amino-terminal homology <PAH>
F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:191-217/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:382-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:440-485/Domain: proteoglycan carboxy-terminal homology <PCR>

Query Match 11.1%; Score 171; DB 2; Length 1091;
Best Local Similarity 23.5%; Pred. No. 0.0013;
Matches 67; Conservative 33; Mismatches 123; Indels 62; Gaps 12;

Qy 37 EVRIENNPNVKSVCASVSGSSP-RVEMKPDQDITRLVYNNKKTASVDRITPPT 96
Db 37 EVRIENNPNVKSVCASVSGSSP-RVEMKPDQDITRLVYNNKKTASVDRITPPT 96

Db 609 DIAIRGTGTALECAATGHPNPQIAWKDGG-----TDFPARERRRMHVMDDVDF 659
Qy 97 --KSYTRDPTGTTCMVSEEGNSYGEVKV--LIVLPSPKPTVINISSATIGNRAVL 152
Db 660 FITDVKIDDMGVYSGTAQ-----NSAGSVANATLVLETPLSLAVPLEDRVYVGTVAEQ 715
Qy 153 CSBODGSPSEYTWFKDGIWPTNPKSTRAFSNSYVNLPTTGELVPPLASDPTGESC 212
Db 716 C-KATGSTPPTITMKGG-----RPLSL-----TERHHTFGNQLLVQNMIMDDGRYTC 765
Qy 213 EARNYGTPMTSNAYRMEAVE-----RNVGYVAALVTILIGILVFGIWFMA----- 260
Db 766 EMSNPLGTERASHQSILPTPGCRKDGTTGCIPTLAVCSIVLTSL-----VWVCIIYQTR 821
Qy 261 ----YSRGHFDR-----KKGTSSKKVIYISGPSARSEG 289
Db 822 KSEERYSVTNMTDETIVPPDPVPSYLSQGLTSLDR--QETVVRTEG 863

RESULT 13

C42632
cell adhesion molecule aPCAM (clone d12) - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C42632
R:Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A:Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic A:Reference number: A42632; MUID:92263095; PMID:1585176
A:Accession: C42632
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-765 <MAY>
A:Cross-reference: UNIPROT:Q9TWA4; UNIPARC:UPI000007CFAF
A:Experimental source: CNS
A:Note: sequence extracted from NCBI backbone (NCBI:P10351)
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match 11.0%; Score 169.5; DB 2; Length 765;
Best Local Similarity 25.1%; Pred. No. 0.00011;
Matches 58; Conservative 36; Mismatches 86; Indels 51; Gaps 11;

Qy 9 RKLCLFLT-----AILCSLALGSTVYSSRPVRIENNPNVKSVCASVG 54
Db 189 KKVLCDIIVDTGETKDFYIDFTVVKLPTIAL-PPTHPDNPKV---GDEVKLTQATG 243
Qy 55 FSPSPREVWPKPDGD---TTRLVYNNKKTASVEDRVTELPGITFKSVTRDPTGTTCMV 111
Db 244 VPPF--TYQFKKGDVMTDEVN--NNGV-----LTINPLKTTDQATYTCTA 285
Qy 112 SEEGNSYGEVKVLTIVLPSPKPTVINISSATIGNRAVLTCSEODGSPSEYTWFKDGI 171
Db 286 TNKGG--FAESSNLTLDVVPPTIEDMEERTYAVSQGLITICTAK-GDPSPSVIKKXGP 342
Qy 172 -----VMPNPNPKSTRAFSNSYVLANPTGE-LVPPLASDPTGESCVA 214
Db 343 QSASTDGVNKGVPYTEKVSQNNDMEKTVAGHMTFKFVTVQDACTYICTA 393

RESULT 14

B42632
cell adhesion molecule aPCAM (clone d15) - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B42632
R:Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A:Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic A:Reference number: A42632; MUID:92263095; PMID:1585176
A:Accession: B42632
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-812 <MAY>

A; Cross-references: UNIPROT:Q9TWA5; UNIPARC:UPI000007CEC1

A;Note: sequence extracted from NCBI backbone (NCBIP:101346)

C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like fold

Query Match 11.04: Score 169.5: DB 2: Length 812:

Query Match	11.04;	Score 169.5;	DB 2;	Length 812;
Post Local Client Path:	05.14;	Prod No 0 00013;		

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BeBc Local Similarity 23.14; Pred. NO: 0.00012;
Matches 5A: Conservative 36; Mismatches 86

```

Matches 58; Conservative 36; Mismatches 86; Indels 51; Gaps 11;

9 RKLCLFIL-----AILLCSLALGVTVHSSPEVRI PENNPVLTSCAYSG 54

Db 189 KKYLCDIIVDTGETKDFYIDFTVKLPITAL-PPTIHPDNPKV-----GDEVKITQQTG 243

0Y 55 FSSPRVEWKFDGD--TTRLVCYNKITASIEDRVTFPLPTGITFKSVTRDGTGTYTCMV 11

Db 244 VPP--TYQFKKGDVMTDENV--NGV-----LTINPLKTYDQATYTCI

QY 112 SEEGNSYGEVKVLIVLPSPKPTVNISSATIGNRAVLTCSQDGSPPSEYTWFKDGI 1711

Db 286 TNKG--FAESSNTLDVKPPTIEDMEETYDAVSGOELTITCTAK-GDPEPSVIWKDGP 3422

QY 172 -----VMPTNPKSTRAFSSSYVLNPTTGE-LVFDPLSASDTGEYSCEA 214

Db 343 Q5ASTDGI VNKGP TYEKG SNQNDME EKTVAQHMT FKPVTYQ DAGTYICTA 393

RESULT 15

A42632

cell adhesion molecule apCAM (clone d19) - California sea hare

C:\species: Aplysia californica (california sea hare)
C:\Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #

C:\Date: 04-Mar-1995 #sequence_18-nov-1994 #seq_change 05-Jul-2004
C:\Acceesion: A42632

R; Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.

Science 256, 638-644, 1992

A; Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plasticity

A:Accession: A42632
A:Reference number: A42632; MUID:92263095; PMID:1585176

A: Status: preliminary; not compared with conceptual tra

A; molecule type: nu

A;Residues: 1-932 <MAY>

A; Cross-references: UNL
A; Experimental source:

A:Note: Sequence extracted from NCBI backbone (NCBIP:1013
A;experimental source: CNS

C;Superfamily: neural cell

Query Match	Score	DB 2;	Length
11.0%;	169.5;	DB 2;	Length 932;

Best Local Similarity 25.1%; Pred. NO. 0.00014;
Matches 58: Conservative 36: Mismatches 86: Indel

DATE	DESCRIPTION	AMOUNT	CHECK NO.	BANK	INITIALS
1/1/50	DEPOSIT	100.00		CHASE	
1/15/50	PAYROLL	50.00	101	CHASE	
1/30/50	RENT	25.00	102	CHASE	
2/1/50	DEPOSIT	150.00		CHASE	
2/15/50	PAYROLL	50.00	103	CHASE	
2/28/50	RENT	25.00	104	CHASE	
3/1/50	DEPOSIT	200.00		CHASE	
3/15/50	PAYROLL	50.00	105	CHASE	
3/30/50	RENT	25.00	106	CHASE	
4/1/50	DEPOSIT	250.00		CHASE	
4/15/50	PAYROLL	50.00	107	CHASE	
4/30/50	RENT	25.00	108	CHASE	
5/1/50	DEPOSIT	300.00		CHASE	
5/15/50	PAYROLL	50.00	109	CHASE	
5/30/50	RENT	25.00	110	CHASE	
6/1/50	DEPOSIT	350.00		CHASE	
6/15/50	PAYROLL	50.00	111	CHASE	
6/30/50	RENT	25.00	112	CHASE	
7/1/50	DEPOSIT	400.00		CHASE	
7/15/50	PAYROLL	50.00	113	CHASE	
7/30/50	RENT	25.00	114	CHASE	
8/1/50	DEPOSIT	450.00		CHASE	
8/15/50	PAYROLL	50.00	115	CHASE	
8/30/50	RENT	25.00	116	CHASE	
9/1/50	DEPOSIT	500.00		CHASE	
9/15/50	PAYROLL	50.00	117	CHASE	
9/30/50	RENT	25.00	118	CHASE	
10/1/50	DEPOSIT	550.00		CHASE	
10/15/50	PAYROLL	50.00	119	CHASE	
10/30/50	RENT	25.00	120	CHASE	
11/1/50	DEPOSIT	600.00		CHASE	
11/15/50	PAYROLL	50.00	121	CHASE	
11/30/50	RENT	25.00	122	CHASE	
12/1/50	DEPOSIT	650.00		CHASE	
12/15/50	PAYROLL	50.00	123	CHASE	
12/30/50	RENT	25.00	124	CHASE	
1/1/51	DEPOSIT	700.00		CHASE	
1/15/51	PAYROLL	50.00	125	CHASE	
1/30/51	RENT	25.00	126	CHASE	
2/1/51	DEPOSIT	750.00		CHASE	
2/15/51	PAYROLL	50.00	127	CHASE	
2/28/51	RENT	25.00	128	CHASE	
3/1/51	DEPOSIT	800.00		CHASE	
3/15/51	PAYROLL	50.00	129	CHASE	
3/30/51	RENT	25.00	130	CHASE	
4/1/51	DEPOSIT	850.00		CHASE	
4/15/51	PAYROLL	50.00	131	CHASE	
4/30/51	RENT	25.00	132	CHASE	
5/1/51	DEPOSIT	900.00		CHASE	
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6/15/51	PAYROLL	50.00	135	CHASE	
6/30/51	RENT	25.00	136	CHASE	
7/1/51	DEPOSIT	1000.00		CHASE	
7/15/51	PAYROLL	50.00	137	CHASE	
7/30/51	RENT	25.00	138	CHASE	
8/1/51	DEPOSIT	1050.00		CHASE	
8/15/51	PAYROLL	50.00	139	CHASE	
8/30/51	RENT	25.00	140	CHASE	
9/1/51	DEPOSIT	1100.00		CHASE	
9/15/51	PAYROLL	50.00	141	CHASE	
9/30/51	RENT	25.00	142	CHASE	
10/1/51	DEPOSIT	1150.00		CHASE	
10/15/51	PAYROLL	50.00	143	CHASE	
10/30/51	RENT	25.00	144	CHASE	
11/1/51	DEPOSIT	1200.00		CHASE	
11/15/51	PAYROLL	50.00	145	CHASE	
11/30/51	RE				

9 RKLCLFIL-----ALLCSLAGSVTH

[illegible]

55 FSSPBYEWKEDCD--TTBIWYNNKTTASVENDVTEIPTGITEKSVTPEDTGTVMV 11

[illegible]

0-9

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

.. .. .

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QY 172 -----VMP TNP KSTRA FSNSS YVLN PTTGE-LVFDPLS ASDTGEYSCEA 214

Db 343 QSASTDGI VNKGPTEKVGSNQNDMEKTV AQHMTFKPVTYQDAGTYICTA 393

Search completed: May 16, 2006, 07:03:28
Job time : 64 secs

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OM protein - protein search, using sw model
Run on: May 16, 2006, 07:03:43 ; Search time 187 Seconds
(without alignments)
702.536 Million cell updates/sec

Title: US-10-785-433-1
Perfect score: 1544
Sequence: 1 MGTAQVERKLLCLFILAIL.....YSPSARSEGFKQTSSFLV 299
Scoring table: GAPDP 10.0 , GAPexp 0.5
2443163
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseqp1980s:*
A: Geneseq_21:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV23321	standard;	protein;	299	AA.	
DE	Amino acid	sequence	of the	PRO301	polypeptide.	
PN	WO927098-A2.					
PD	03-JUN-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 1544;	DB 2;	Length 299;	
Best Local Similarity		100.0%;	Pred. No. 7.5e-105;			
RESULT 2						
ID	AAW74464	standard;	protein;	299	AA.	
DE	F11 antigen	protein	sequence.			
PN	WO9902561-A1.					
PD	21-JAN-1999.					
PA	(SMIK) SMITHKLINE BEECHAM CORP.					
Query Match		100.0%;	Score 1544;	DB 2;	Length 299;	
Best Local Similarity		100.0%;	Pred. No. 7.5e-105;			
RESULT 3						
ID	AAV13364	standard;	protein;	299	AA.	
DE	Amino acid	sequence	of protein	PRO301.		
PN	WO9914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 1544;	DB 2;	Length 299;	
Best Local Similarity		100.0%;	Pred. No. 7.5e-105;			
RESULT 4						
ID	AAV76011	standard;	protein;	299	AA.	
DE	Human A33	receptor	homologue, SEQ ID NO:189.			
PN	WO9955865-A1.					
PD	04-NOV-1999.					
PA	(GENE-) GENESIS RES & DEV CORP LTD.					
Query Match		100.0%;	Score 1544;	DB 3;	Length 299;	
Best Local Similarity		100.0%;	Pred. No. 7.5e-105;			
RESULT 5						
ID	AAV76076	standard;	protein;	299	AA.	
DE	Human A33	receptor	homologue, SEQ ID NO:331.			
PN	WO9955865-A1.					
PD	04-NOV-1999.					
PA	(GENE-) GENESIS RES & DEV CORP LTD.					
Query Match		100.0%;	Score 1544;	DB 3;	Length 299;	
Best Local Similarity		100.0%;	Pred. No. 7.5e-105;			
RESULT 6						
ID	AAV70670	standard;	protein;	299	AA.	
DE	Human PRO301	protein.				

PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0% ; Score 1544; DB 3; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 7
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0% ; Score 1544; DB 3; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 8
ID AAV93344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0% ; Score 1544; DB 3; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 9
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0% ; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 10
ID AAM93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 100.0% ; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 11
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 100.0% ; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 12
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 100.0% ; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 13
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0% ; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 14
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0% ; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0% ; Pred. No. 7.5e-105;

RESULT 15
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.

PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 16
ID AAB53086 standard; protein: 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN W0200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 17
ID AAU14405 standard; protein: 299 AA.
DE Human novel protein #276.
PN W0200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 18
ID AAU14404 standard; protein: 299 AA.
DE Human novel protein #275.
PN W0200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 19
ID AAU14168 standard; protein: 299 AA.
DE Human novel protein #39.
PN W0200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 20
ID AAE03896 standard; protein: 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN W0200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 21
ID AAE03840 standard; protein: 299 AA.
DE Human gene 23 encoded secreted protein HACA29, SEQ ID NO: 86.
PN W0200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 22
ID AAE03870 standard; protein: 299 AA.
DE Human gene 23 encoded secreted protein HACA29, SEQ ID NO:116.
PN W0200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1544; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 23
ID ABB90290 standard; protein: 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 24
ID ABB84843 standard; protein: 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN W020020690-A2.
PD 03-JAN-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 25
ID ABG64551 standard; protein: 299 AA.
DE Human albumin fusion protein #1226.
PN W0200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 26
ID ABG64552 standard; protein: 299 AA.
DE Human albumin fusion protein #1227.
PN W0200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 27
ID ABB72215 standard; protein: 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN W0200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 28
ID ABB72150 standard; protein: 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN W0200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 29
ID ABB95449 standard; protein: 299 AA.
DE Human angiogenesis related protein PRO301 SEQ ID NO: 54.
PN W0200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1544; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 30
ID ABU71610 standard; protein: 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 31
ID ABC17798 standard; protein: 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;

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Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 32 ID ABU71465 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 33 ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 34 ID ABU81052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 35 ID ABU71911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 36 ID ABO01794 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 37 ID ABU66752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 38 ID ABU54367 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 39 ID ABU67291 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 40 ID ABO47382 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 41 ID ABU59833 standard; protein; 299 AA.
DE Novel secreted and transmembrane protein PRO301.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 42 ID ABO25023 standard; protein; 299 AA.
DE Human secreted/transmembrane protein (PRO) #183.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 43 ID ABU64519 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #23.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 44 ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 45 ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 46 ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 47 ID ABO14885 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 48 ID ABU07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 49 ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (hJAM1).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL ) LILLY & CO ELI.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 50
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ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 51
ID ABU69642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 52
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 53
ID ABO14824 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 54
ID ADA5885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 55
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 56
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 57
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 58
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 59
ID ADB19374 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 60
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 61
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 62
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 63
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 64
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 65
ID ABO32776 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 66
ID ADA67539 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 67
ID ADB30546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 68
ID ADA85842 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 69
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 70
ID ADA9358 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 71
ID ADA87497 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 72
ID ADA16699 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 73
ID ABO34836 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 74
ID ADA16155 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 75
ID ADA91791 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 76
ID ADA14854 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 77
ID ADA47263 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044844-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 78
ID ADB18815 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 79
ID ADA94030 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 80
ID ADB19926 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 81
ID ADB13238 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 82
ID ABO43331 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 83
ID ADA74492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 84
ID ADA42300 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 85
ID ADB24725 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 86
ID ADA82249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082701-A1.
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 87
ID ADA75212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 88
ID ADA85290 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 89
ID ADA84738 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 90
ID ABO17514 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 91
ID ADB29994 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 92
ID ADA80522 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 93
ID ADA75764 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 94
ID ADA46989 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 95
ID ADB25285 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 96
ID ADA93461 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 97
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 98
ID ADB31098 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 99
ID ADA61026 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 100
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 101
ID ADA96502 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 102
ID ADA81074 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 103
ID ADA95950 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 104
ID ADB26259 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
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Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 105
ID ADA21744 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 106
ID ADA77523 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 107
ID ADA18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 108
ID ADA86946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 109
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 110
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 111
ID ADA1876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 112
ID ADA88049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 113
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 114
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 115
ID ADA42726 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 116
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 117
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 118
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 119
ID ADA88601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 120
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 121
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200302239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 122
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 123
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
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PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 124
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 125
ID ADA66987 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 126
ID ADB22848 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 127
ID ADB23621 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 128
ID ADA93243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 129
ID ADB15406 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 130
ID ADB38658 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 131
ID ADB38106 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 132
ID ADB66578 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082689-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 133
ID ADB89658 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 134
ID ADB90390 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 135
ID ADB77645 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 136
ID ADB39491 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 137
ID ADB74781 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 138
ID ADB47114 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 139
ID ADB86721 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 140
ID ADB77326 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 141
ID ADB34483 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077717-A1.
PD 24-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 142
ID ADB35587 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 143
ID ADB33931 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 144
ID ADB35035 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 145
ID ADB36139 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 146
ID ADB46534 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 147
ID ADC28427 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 148
ID ADC39627 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 149
ID ADC40141 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 150
ID ADC18969 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 151
ID ADC34265 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 152
ID ADC29320 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003046576-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 153
ID ADC28851 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 154
ID ADC40736 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 155
ID ADC19393 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 156
ID ADC33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 157
ID ADC12911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 158
ID ADC50407 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 159
ID ADC71954 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
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Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 160
ID ADC5933 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030923105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 161
ID ADC52940 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 162
ID ADC57294 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 163
ID ADC60485 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 164
ID ADC50960 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 165
ID ADC65487 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 166
ID ADC54585 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 167
ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 168
ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 169
ID ADC5947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 170
ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 171
ID ADC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 172
ID ADD03191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 173
ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 174
ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 175
ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 176
ID ADD10020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 177
ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 178

ID ADC60551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 179
ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 180
ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 181
ID ADC47939 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 182
ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 183
ID ADC79999 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 184
ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 185
ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 186
ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 187
ID ADD03500 standard; protein; 299 AA.

DE Human secreted/transmembrane protein, #25.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 188
ID ADD11181 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 189
ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 190
ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 191
ID ADD53612 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 192
ID ADD37096 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 193
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 194
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 195
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 196
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 197
ID ADE92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 198
ID ADE91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 199
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 200
ID ADE32307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 201
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 202
ID ADE79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 203
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 204
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 205
ID ADE91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 206
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 207
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 208
ID ADE80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 209
ID ADE93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 210
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 211
ID ADE34752 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 212
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 213
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 214
ID ADE95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199059-A1.
PD 23-OCT-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 215
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 216
ID ADJ78909 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 217
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 218
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 219
ID ADH80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 220
ID ADH89595 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 221
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 222
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 223
ID ADH92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 224
ID ADG21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 225
ID ADG31517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 226
ID ADP97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 227
ID ADG80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 228
ID ADG80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 229
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 230
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUNA/) TUNAS D.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 231
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 232
ID ADH92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 233
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ID ADH55296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 233
ID ADH5548 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 234
ID ADI38014 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 235
ID ADI6467 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 236
ID ADI65016 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 237
ID ADI6315 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 238
ID ADH8129 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 239
ID ADH8137 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 240
ID ADJ26282 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 241
ID ADM82546 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 242
ID ADN15945 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 243
ID ADN16574 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 244
ID ADN15393 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 245
ID ADN14841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 246
ID ADG81103 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 247
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 248
ID ADD76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 249
ID ADD87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 250
ID ADD86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 251
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 252
ID ADE75767 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 253
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 254
ID ADE41304 standard; protein; 299 AA.
DE Human secreted/cranmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 255
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 256
ID ADE23895 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 257
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 258
ID ADE87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 259
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 260
ID ADE41186 standard; protein; 299 AA.
DE Human secreted/cranmembrane polypeptide PRO301.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 261
ID ADE73832 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 262
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 263
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 264
ID ADE93936 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 265
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 266
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 267
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 268
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 269
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 270
ID ADE98505 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 271
ID ADE92255 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 272
ID ADE90556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 273
ID ADE91703 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 274
ID ADE98932 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 275
ID ADG40402 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 276
ID ADF73796 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 277
ID ADG02282 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 278
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 279
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 280
ID ADF98044 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 281
ID ADG24261 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 282
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 283
ID ADG03446 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 284
ID ADF99167 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 285
ID ADG16752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 286

ID ADG05211 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 287
ID ADG19478 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 288
ID ADG73372 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003165051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 289
ID ADG13315 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 290
ID ADG08372 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 291
ID ADG15542 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 292
ID ADG96940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 293
ID ADG06125 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 294
ID ADG23709 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 295
ID ADG03998 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 296
ID ADG24899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 297
ID ADG07196 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 298
ID ADG07748 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 299
ID ADG55243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 300
ID ADG60907 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 301
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 302
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003207145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 303
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 304
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 305
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 306
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 307
ID ADG58555 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 308
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 309
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003207146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 310
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 311
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 312
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 313
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 314
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 315
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 316
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 317
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 318
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 319
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 320
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 321
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 322
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 323
ID ADH28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 324
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200307367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 325
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200307369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 326
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 327
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US200324984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 328
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 329
ID ADH59831 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 330
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (GURN/) GURNEY A L.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 331
ID ADH1155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 332
ID ADH18601 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 333
ID ADI65321 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 334
ID ADI37584 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 335
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 336
ID ADH97380 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 337
ID ADI15369 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200307382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 338
ID ADG09246 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 339
ID ADI65748 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003148371-A1.
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PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 340
ID AD114701 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 341
ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 342
ID AD118296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 343
ID ADJ95948 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 344
ID ADL08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 345
ID AD147176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 346
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 347
ID ADK40844 standard; protein; 299 AA.
DE Human platelet P11 receptor #1.
PN US669688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 100.0%; Score 1544; DB 8; Length 299;

Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 348
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 349
ID ADM29632 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 350
ID ADL77818 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 351
ID ADL77819 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 352
ID ADJ77472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 353
ID ADK82832 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 354
ID ADJ65594 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 355
ID ADL31332 standard; protein; 299 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3365.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 356
ID ADM27730 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 357				
ID ADL26800 standard; protein; 299 AA.				
DE Human JAM1 protein SRQ ID NO:54.				
PN WO2004022778-A1.				
PD 18-MAR-2004.				
PA (GARV-) GANVAN INST MEDICAL RES.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 358				
ID ADM42454 standard; protein; 299 AA.				
DE Human PRO polypeptide #183.				
PN US2004058424-A1.				
PD 25-MAR-2004.				
PA (GETH-) GENENTECH INC.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 359				
ID AD006154 standard; protein; 299 AA.				
DE Human PRO polypeptide #21.				
PN US6686451-B1.				
PD 03-FEB-2004.				
PA (GETH-) GENENTECH INC.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 360				
ID ADN35284 standard; protein; 299 AA.				
DE Human PRO301 protein.				
PN WO2004031105-A2.				
PD 15-APR-2004.				
PA (GETH-) GENENTECH INC.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 361				
ID ADN05140 standard; protein; 299 AA.				
DE Antipsoiatic protein sequence #749.				
PN WO2004028479-A2.				
PD 08-APR-2004.				
PA (GETH-) GENENTECH INC.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 362				
ID ADM28316 standard; protein; 299 AA.				
DE Human PRO polypeptide #183.				
PN US2004077054-A1.				
PD 22-APR-2004.				
PA (GETH-) GENENTECH INC.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 363				
ID AD095890 standard; protein; 299 AA.				
DE T cell activation associated protein #34.				
PN WO2004058805-A2.				
PD 15-JUL-2004.				
PA (ASAH-) ASAH KASEI PHARMA CORP.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 364				
ID ADRI1006 standard; protein; 299 AA.				
DE Human secreted/transmembrane protein, #25.				
PN US2004137561-A1.				
PD 15-JUL-2004.				
PA (GETH-) GENENTECH INC.				
Query Match	100.0%;	Score 1544;	DB 8;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 7.5e-105;		
RESULT 365				
ID ADRI7915 standard; protein; 299 AA.				
DE Human secreted/transmembrane protein, #25.				
PN US2004147017-A1.				
PD 29-JUL-2004.				
PA (ASHK/) ASHKENAZI A.				
PA (BOTS/) BOTSTEIN D.				

PA	(DESN//)	DESNOYERS L.
PA	(EATO//)	EATON D L.
PA	(FERR//)	FERRARA N.
PA	(FILV//)	FILVAROFF E.
PA	(FONG//)	FONG S.
PA	(GNOW//)	GNO W.
PA	(GERB//)	GERBER H.
PA	(GERR//)	GERRITSEN M E.
PA	(GODD//)	GODDARD A.
PA	(GODO//)	GODOWSKI P J.
PA	(GRIM//)	GRIMALDI C J.
PA	(GURN//)	GURNEY A L.
PA	(HILL//)	HILLMAN K J.
PA	(KLJA//)	KLJAVIN I J.
PA	(MATH//)	MATHER J P.
PA	(PANU//)	PAN J.
PA	(PAONI//)	PAONI N F.
PA	(ROYM//)	ROY M A.
PA	(STEM//)	STEWART T A.
PA	(TUMA//)	TUMAS D.
PA	(WILL//)	WILLIAMS P M.
PA	(WOOD//)	WOOD W I.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 366		
ID	ADR27641 standard; protein; 299 AA.	
DE	Human Fil receptor protein Seq 7.	
PN	WO2004063327-A2.	
PD	29-JUL-2004.	
PA	(KORN//)	KORNECKI E.
PA	(BAB1//)	BABINSKA A.
PA	(EHRL//)	EHRLICH Y H.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 367		
ID	ADI95798 standard; protein; 299 AA.	
DE	Human PRO polypeptide #183.	
PN	US2003077659-A1.	
PD	24-APR-2003.	
PA	(GEHT//)	GENENTECH INC.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 368		
ID	ADI96350 standard; protein; 299 AA.	
DE	Novel human secreted and transmembrane protein PRO301.	
PN	US2003023754-A1.	
PD	06-NOV-2003.	
PA	(GEHT//)	GENENTECH INC.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 369		
ID	ADP46577 standard; protein; 299 AA.	
DE	Human JAM-1, Fil receptor (F1IR) transcript variant 4, SEQ ID 8	
PN	JF2004242513-A.	
PD	02-SEP-2004.	
PA	(DOKU//)	DOKURITSU GYOSEI HOJIN KAGAKU GIUTSU SH.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 370		
ID	ADN446571 standard; protein; 299 AA.	
DE	Human JAM-1, Fil receptor (F1IR) transcript variant 4.	
PN	JF2004242513-A.	
PD	02-SEP-2004.	
PA	(DOKU//)	DOKURITSU GYOSEI HOJIN KAGAKU GIUTSU SH.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 371		
ID	ADR46573 standard; protein; 299 AA.	
DE	Human JAM-1, Fil receptor (F1IR) transcript variant 4.	
PN	JF2004242513-A.	
PD	02-SEP-2004.	
PA	(DOKU//)	DOKURITSU GYOSEI HOJIN KAGAKU GIUTSU SH.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;
RESULT 372		
ID	ADP46573 standard; protein; 299 AA.	
DE	Human JAM-1, Fil receptor (F1IR) transcript variant 4.	
PN	JF2004242513-A.	
PD	02-SEP-2004.	
PA	(DOKU//)	DOKURITSU GYOSEI HOJIN KAGAKU GIUTSU SH.
Query Match		
	Best Local Similarity	100.0%; Score 1544; DB 8; Length 299;
		100.0%; Pred. No.7.5e-105;

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Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 372
ID ADR46579 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcrit variant 5.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (BOOK-) DOKURITSU GYOSEI HOJIN KAGAKU GIYUTSU SH.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 373
ID ADR94260 standard; protein; 299 AA.
DE Human PRO301 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GERTH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 374
ID ADS74554 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein #25.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 375
ID ADS32302 standard; protein; 299 AA.
DE Novel human secreted and cranmembrane protein PRO301.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GERTH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 376
ID ADU03286 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GERTH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 377
ID ADU03591 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GERTH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 378
ID ADU06480 standard; protein; 299 AA.
DE Novel bronchial cancer-associated human protein SegID704.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 379
ID ADU06355 standard; protein; 299 AA.
DE Novel bronchial cancer-associated human protein SegID579.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 380
ID ADU66684 standard; protein; 299 AA.
DE Human platelet F11 receptor protein, F11R-A.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
Pred. No. 7.5e-105;
RESULT 381
ID ADW97860 standard; protein; 299 AA.
DE Human junctional adhesion molecule-1 (JAM-1) protein.
PN US2005025776-A1.
PD 03-FEB-2005.
PA (WEBE/) WEBER C.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 299;
Pred. No. 7.5e-105;
RESULT 382
ID ADZ03337 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein PRO301 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GERTH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 299;
Pred. No. 7.5e-105;
RESULT 383
ID AEA37829 standard; protein; 299 AA.
DE Human secreted/cranmembrane protein, #25.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GERTH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 299;
Pred. No. 7.5e-105;
RESULT 384
ID AEA29245 standard; protein; 299 AA.
DE Human junction adhesion molecule -1 as target for drug delivery method.
PN US2005129679-A1.
PD 16-JUN-2005.
PA (NAST-) NASTECH PHARM CO INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 299;
Pred. No. 7.5e-105;
RESULT 385
ID AEB14083 standard; protein; 299 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 366.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERSINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
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PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 299;
Pred. No. 7.5e-105;
RESULT 386
ID AD509073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 7; Length 320;
Pred. No. 8.1e-105;
RESULT 387
ID ADU40591 standard; protein; 320 AA.
DE Novel human polypeptide seq id 376.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 320;
Pred. No. 8.1e-105;
RESULT 388
ID AD808038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 7; Length 336;
Pred. No. 8.6e-105;
RESULT 389
ID ADU40408 standard; protein; 336 AA.
DE Novel human polypeptide seq id 193.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 100.0%; Score 1544; DB 9; Length 336;
Pred. No. 8.6e-105;
RESULT 390
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 99.7%; Score 1540; DB 2; Length 299;
Pred. No. 1.5e-104;
RESULT 391
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 99.7%; Score 1539; DB 3; Length 299;
Pred. No. 1.7e-104;
RESULT 392
ID ADH80723 standard; protein; 300 AA.
DE Human polypeptide #40.
PN US200332054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 98.5%; Score 1521.5; DB 8; Length 300;
Pred. No. 3.3e-103;
RESULT 393
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US200332054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 97.5%; Score 1505; DB 8; Length 301;
Pred. No. 5.4e-102;
RESULT 394
ID AD67617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 97.2%; Score 1500; DB 8; Length 351;
Pred. No. 1.5e-101;
RESULT 395
ID AD67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 91.4%; Score 1411; DB 8; Length 335;
Pred. No. 4.6e-95;
RESULT 396
ID AAU17996 standard; protein; 301 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 141.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 90.4%; Score 1396.5; DB 4; Length 301;
Pred. No. 4.7e-94;
RESULT 397
ID ABB10232 standard; protein; 301 AA.
DE Human cDNA SEQ ID NO: 540.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 92.0%; Score 1396.5; DB 4; Length 301;
Pred. No. 4.7e-94;
RESULT 398
ID ABP66819 standard; protein; 301 AA.
DE Human polypeptide SEQ ID NO 540.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 90.4%; Score 1396.5; DB 5; Length 301;
Pred. No. 4.7e-94;
RESULT 399
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ID ADB31620 standard; protein; 301 AA.
DE Human novel protein SEQ ID NO 141.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 90.4%; Score 1396.5; DB 7; Length 301;
Best Local Similarity 92.0%; Pred. No. 4.7e-94;
RESULT 400
ID ADR41522 standard; protein; 318 AA.
DE Human CD-like molecule HKAC103, SEQ ID NO:321.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 90.4%; Score 1396.5; DB 5; Length 318;
Best Local Similarity 92.0%; Pred. No. 5e-94;
RESULT 401
ID AAW61379 standard; protein; 298 AA.
DE Human junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOPF) HOFFMANN LA ROCHE & CO AG F.
Query Match 89.5%; Score 1382.5; DB 2; Length 298;
Best Local Similarity 91.0%; Pred. No. 4.9e-93;
RESULT 402
ID AAY33328 standard; protein; 263 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GERTH) GENENTECH INC.
Query Match 88.9%; Score 1372; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.5e-92;
RESULT 403
ID AAY08074 standard; protein; 263 AA.
DE Human DNA0628 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GERTH) GENENTECH INC.
Query Match 88.9%; Score 1372; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.5e-92;
RESULT 404
ID ADH62552 standard; protein; 263 AA.
DE Human PRO301 protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 88.9%; Score 1372; DB 7; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.5e-92;
RESULT 405
ID AAY33326 standard; protein; 260 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GERTH) GENENTECH INC.
Query Match 87.8%; Score 1355; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 4.3e-91;
RESULT 406
ID AAY08072 standard; protein; 260 AA.
DE Human DNA40628 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GERTH) GENENTECH INC.
Query Match 87.8%; Score 1355; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 4.3e-91;
RESULT 407
ID ADH62550 standard; protein; 260 AA.
DE Human PRO301 protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 87.8%; Score 1355; DB 7; Length 260;
Best Local Similarity 100.0%; Pred. No. 4.3e-91;
RESULT 408
ID ADQ95892 standard; protein; 259 AA.
DE T cell activation associated protein #35.
PN WO2004058805-A2.
PD 15-JUN-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 83.4%; Score 1287; DB 8; Length 259;
Best Local Similarity 86.3%; Pred. No. 4.1e-86;
RESULT 409
ID ADR46575 standard; protein; 259 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 3.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOUJIN KAGAKU GIYUTSU SH.
Query Match 83.4%; Score 1287; DB 8; Length 259;
Best Local Similarity 86.3%; Pred. No. 4.1e-86;
RESULT 410
ID AAU14169 standard; protein; 259 AA.
DE Human novel protein #40.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 83.0%; Score 1281; DB 4; Length 259;
Best Local Similarity 86.0%; Pred. No. 1.1e-85;
RESULT 411
ID ABU69130 standard; protein; 225 AA.
DE Human NOVX polypeptide #5.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 72.2%; Score 1114; DB 6; Length 225;
Best Local Similarity 75.3%; Pred. No. 1.6e-73;
RESULT 412
ID ADO08263 standard; protein; 225 AA.
DE Human NOVX polypeptide #5.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASW/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LITX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATURAJAN M.
PA (PENNA) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
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PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERN/) ZERNHSEN B D.
Query Match 72.2%; Score 1114; DB 8; Length 225;
Best Local Similarity 75.3%; Pred. No. 1.6e-73;
RESULT 413
ID AD846581 standard; protein: 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN UP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIYUTSU SH.
Query Match 69.9%; Score 1079.5; DB 8; Length 300;
Best Local Similarity 68.4%; Pred. No. 7.5e-71;
RESULT 414
ID AAM61380 standard; protein: 300 AA.
DE Mouse junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 69.5%; Score 1073.5; DB 2; Length 300;
Best Local Similarity 68.1%; Pred. No. 2.1e-70;
RESULT 415
ID AAY23325 standard; protein: 300 AA.
DE A33 related antigen JAM.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 69.5%; Score 1073.5; DB 2; Length 300;
Best Local Similarity 68.1%; Pred. No. 2.1e-70;
RESULT 416
ID ADH62537 standard; protein: 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 69.5%; Score 1073.5; DB 7; Length 300;
Best Local Similarity 68.1%; Pred. No. 2.1e-70;
RESULT 417
ID ADX40853 standard; protein: 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US669688-B1.
PD 02-MAR-2004.
PA (UTNY) UNIV NEW YORK STATE RES FOUND.
Query Match 69.5%; Score 1073.5; DB 8; Length 300;
Best Local Similarity 68.1%; Pred. No. 2.1e-70;
RESULT 418
ID ADN35293 standard; protein: 300 AA.
DE Human JAM protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 69.5%; Score 1073.5; DB 8; Length 300;
Best Local Similarity 68.1%; Pred. No. 2.1e-70;
RESULT 419
ID ADU66693 standard; protein: 300 AA.
DE Mouse junctional adhesion molecule (JAM).
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 69.5%; Score 1073.5; DB 8; Length 300;
Best Local Similarity 68.1%; Pred. No. 2.1e-70;
RESULT 420
ID AAM74465 standard; protein: 205 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.

PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 67.5%; Score 1042.5; DB 2; Length 205;
Best Local Similarity 98.5%; Pred. No. 2.5e-68;
RESULT 421
ID AAB39253 standard; protein: 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 67.2%; Score 1038; DB 3; Length 280;
Best Local Similarity 69.9%; Pred. No. 7.6e-68;
RESULT 422
ID ADK40845 standard; protein: 193 AA.
DE Human platelet F11 receptor #2.
PN US669688-B1.
PD 02-MAR-2004.
PA (UTNY) UNIV NEW YORK STATE RES FOUND.
Query Match 58.9%; Score 910; DB 8; Length 193;
Best Local Similarity 97.2%; Pred. No. 1.1e-58;
RESULT 423
ID ADU66685 standard; protein: 193 AA.
DE Human platelet F11 receptor protein, F11R-B.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 58.9%; Score 910; DB 8; Length 193;
Best Local Similarity 97.2%; Pred. No. 1.1e-58;
RESULT 424
ID AAY75995 standard; protein: 134 AA.
DE Human skin cell protein, SEQ ID NO:173.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 37.3%; Score 576; DB 3; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
RESULT 425
ID AAB55934 standard; protein: 134 AA.
DE Skin cell protein, SEQ ID NO: 173.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 37.3%; Score 576; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
RESULT 426
ID ABB72134 standard; protein: 134 AA.
DE Human protein isolated from skin cells SEQ ID NO: 173.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 37.3%; Score 576; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.1e-34;
RESULT 427
ID AAU18030 standard; protein: 141 AA.
DE Human immunoglobulin polypeptide SEQ ID No 175.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.0%; Score 525; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 428
ID AAM94741 standard; protein: 141 AA.
DE Human reproductive system related antigen SEQ ID NO: 3399.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.0%; Score 525; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 429
ID ABB10228 standard; protein: 141 AA.
DE Human cDNA SEQ ID NO: 536.
PN WO200154474-A2.
PD 02-AUG-2001.

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PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.0%; Score 525; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 430
ID AAU22763 standard; protein; 141 AA.
DE Human prostate cancer antigen, Seq ID No 282.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.0%; Score 525; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 431
ID ABP6815 standard; protein; 141 AA.
DE Human polypeptide seq ID NO 596.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 34.0%; Score 525; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 432
ID ADB31654 standard; protein; 141 AA.
DE Human novel protein SEQ ID NO 175.
PN US200307606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.0%; Score 525; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 433
ID ADU09336 standard; protein; 141 AA.
DE Human prostate cancer associated polypeptide SeqID282.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.0%; Score 525; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
RESULT 434
ID ADM97861 standard; protein; 88 AA.
DE Human JAM-1 protein active fragment.
PN US2005025776-A1.
PD 03-FEB-2005.
PA (WEBE/) WEBER C.
Query Match 30.0%; Score 463; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.4e-26;
RESULT 435
ID AAM85457 standard; protein; 298 AA.
DE Secreted protein encoded by clone c864_4.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMT/) GENETICS INST INC.
Query Match 27.9%; Score 431; DB 2; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 436
ID AAU0512 standard; protein; 298 AA.
DE Human junctional adhesion protein (JAM2).
PN WO200114404-A1.
PD 01-MAR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 27.9%; Score 431; DB 4; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 437
ID ABP61801 standard; protein; 298 AA.
DE Human polypeptide seq ID NO 155.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLE E R.
PA (COLL/) COLLINS-RACTE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 27.9%; Score 431; DB 5; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 438
ID ABR58532 standard; protein; 298 AA.
DE Human vascular endothelial junction-associated molecule protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 27.9%; Score 431; DB 6; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 439
ID ADI47178 standard; protein; 298 AA.
DE Human JAM-3 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 27.9%; Score 431; DB 8; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 440
ID ADP56681 standard; protein; 298 AA.
DE Human junction adhesion molecule 2 (hJAM2) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL/) LILLY & CO ELI.
Query Match 27.9%; Score 431; DB 8; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 441
ID ABR82288 standard; protein; 298 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO28687, SEQ:5880.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH/) GENENTECH INC.
Query Match 27.9%; Score 431; DB 8; Length 298;
Best Local Similarity 35.3%; Pred. No. 2.2e-23;
RESULT 442
ID AAW75220 standard; protein; 298 AA.
DE Human secreted protein encoded by gene 25 clone HTEB42.
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.8%; Score 429; DB 2; Length 298;
Best Local Similarity 34.2%; Pred. No. 3.1e-23;
RESULT 443
ID AAE26983 standard; protein; 298 AA.
DE Human gene 25 encoded secreted protein HTEB42, SEQ ID NO:76.
PN US2002077287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LITY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (PERR/) FERRIE A M.
Query Match 27.8%; Score 429; DB 5; Length 298;
Best Local Similarity 34.2%; Pred. No. 3.1e-23;
RESULT 444
ID AAE27121 standard; protein; 298 AA.
DE Human gene 25 encoded secreted protein HTEB42, SEQ ID NO:76.
PN US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LITY/) LI Y.
PA (ZENG/) ZENG Z.
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PA (KYAW/) KYAW H.
PA (FISCH/) FISCHER C L.
PA (LITH/) LI H.
PA (SOP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 445
ID ABR47926 standard; protein; 298 AA.
DE Human secreted protein, SEQ ID 817.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 446
ID ABR00172 standard; protein; 298 AA.
DE Human gene 162 encoded secreted protein HTEEB42, SEQ ID NO:461.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 447
ID ABU6494 standard; protein; 298 AA.
DE Human secreted protein gene 25, protein.
PN US2002172994-A1.
PD 21-NOV-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LITY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LITH/) LI H.
PA (SOP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 448
ID ADB91670 standard; protein; 298 AA.
DE Human secreted protein #SEQ ID 616.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 449
ID ADC74331 standard; protein; 298 AA.
DE Human secreted protein - SEQ ID 964.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 450
ID ADG89803 standard; protein; 298 AA.
DE Human protein from secreted protein gene 25.
PN US200325009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) ROSEN S M.
PA (LITY/) LI Y.

PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LITH/) LI H.
PA (SOP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
Query Match
Best Local Similarity 34.2%; Pred. No. 3.1e-23; Length 298;
RESULT 451
ID AAO16452 standard; protein; 298 AA.
DE Human junctional adhesion molecule 2 (hujAM2).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (EILY) LILLY & CO ELI.
Query Match
Best Local Similarity 38.3%; Pred. No. 3.6e-23; Length 298;
RESULT 452
ID AAO16453 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (hujAM3).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (EILY) LILLY & CO ELI.
Query Match
Best Local Similarity 32.8%; Pred. No. 4.5e-23; Length 310;
RESULT 453
ID AAY96735 standard; protein; 310 AA.
DE PRO1868, an A33 antigen homologue.
PN WO200036102-A2.
PD 22-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23; Length 310;
RESULT 454
ID AAB33457 standard; protein; 310 AA.
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23; Length 310;
RESULT 455
ID AAB27276 standard; protein; 310 AA.
DE Human confuency regulated adhesion molecule 1 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23; Length 310;
RESULT 456
ID AAB80272 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23; Length 310;
RESULT 457
ID AAM93905 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 4051.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23; Length 310;
RESULT 458
ID AAM93323 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.

[illegible][illegible]

Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 484		
ID	ABU54407 standard; protein; 310 AA.	
DE	Human secreted/transmembrane protein PRO1868.	
PN	US2002132240-A1.	
PD	19-SEP-2002.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 485		
ID	ABO47422 standard; protein; 310 AA.	
DE	Human secreted/transmembrane polypeptide PRO1868.	
PN	US2003044839-A1.	
PD	06-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 486		
ID	ABG7314 standard; protein; 310 AA.	
DE	Human PRO1868 polypeptide.	
PN	US2002164646-A1.	
PD	07-NOV-2002.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 487		
ID	ABU59919 standard; protein; 310 AA.	
DE	Novel secreted and transmembrane protein PRO1868.	
PN	US2003017563-A1.	
PD	23-JAN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 488		
ID	ABO25109 standard; protein; 310 AA.	
DE	Human secreted/transmembrane protein (PRO) #269.	
PN	US2003036179-A1.	
PD	20-FEB-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 489		
ID	ABU64559 standard; protein; 310 AA.	
DE	Human secreted/transmembrane protein, #63.	
PN	US2002160374-A1.	
PD	31-OCT-2002.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 490		
ID	ABU67405 standard; protein; 310 AA.	
DE	Human secreted protein PRO1868.	
PN	US2003023054-A1.	
PD	30-JAN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 491		
ID	ABO14925 standard; protein; 310 AA.	
DE	Human secreted / transmembrane polypeptide PRO1868.	
PN	US2003036060-A1.	
PD	20-FEB-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 492		
ID	ABU60813 standard; protein; 310 AA.	
DE	Human secreted/transmembrane protein, #7.	
PN	US2002160392-A1.	
PD	31-OCT-2002.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;
RESULT 493		
ID	ABU60813 standard; protein; 310 AA.	
DE	Human secreted/transmembrane protein, #7.	
PN	US2002160392-A1.	
PD	31-OCT-2002.	
PA	(GETH) GENENTECH INC.	
Query Match	27.5%;	Score 424; DB 6; Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;

RESULT 493
ID AB067114 standard; protein; 310 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 538.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 494
ID AB081236 standard; protein; 310 AA.
DE Human PRO1917polypeptide.
PN US2003032060-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 495
ID AB069682 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868+H30.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 496
ID AB014864 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 497
ID ADA46057 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 498
ID ADA76488 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 499
ID ADB29627 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 500
ID ADA19138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 501
ID ADA61761 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 502
ID ADA86014 standard; protein; 310 AA.

ID ADB19546 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 503
ID ADB28087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 504
ID ADA86566 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 505
ID ADB16130 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 506
ID ADA47916 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 507
ID ADA18484 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 508
ID ABO32816 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 509
ID ADA67711 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 510
ID ADB30718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 511
ID ADA86014 standard; protein; 310 AA.

DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 512
ID ADA97226 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 513
ID ADA79530 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 514
ID ADA87669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 515
ID ADB16871 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 516
ID ABO34876 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 517
ID ADA16459 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 518
ID ADA91963 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 519
ID ADB15026 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 520
ID ADB18987 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 521
ID ADA94202 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 522
ID ADB20098 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 523
ID ADB13410 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 524
ID ABO43417 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 525
ID ADA74664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 526
ID ADA42604 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 527
ID ADB24897 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 528
ID ADA82421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 529
ID ADA75384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073216-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 530
ID ADB85462 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 531
ID ADB48910 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 532
ID ADB017554 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 533
ID ADB30166 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 534
ID ADB06094 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 535
ID ADA75936 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 536
ID ADA47161 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 537
ID ADB25457 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 538
ID ADA93633 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 540
ID ADB31270 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 541
ID ADB62957 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003054447-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 542
ID ADA61198 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 543
ID ADB24345 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 536.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 544
ID ADA96674 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 545
ID ADA81246 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 546
ID ADA96122 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 547
ID ADB26431 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match          27.5%  Score 424; DB 6; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 548
ID AD821916 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 6; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 549
ID ADA76695 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 550
ID ADB18435 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 551
ID ADA87118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 552
ID ADA16883 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 553
ID ADA13312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 554
ID ADA42180 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 555
ID ADA88221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 556
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 557
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 558
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 559
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 560
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 561
ID ABO01894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 562
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 563
ID ADA8773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003072313-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 564
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 565
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          27.5%  Score 424; DB 7; Length 310;
Best Local Similarity 32.8%  Pred. No. 7.5e-23;
RESULT 566
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ID ADB2468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 567
ID ABO17615 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 568
ID ADB67159 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 569
ID ADB23020 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 570
ID ADB23793 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 571
ID ADB92515 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 572
ID ADB15578 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 573
ID ADB38630 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 574
ID ADB38278 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 575
ID ADB66750 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003077717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 576
ID ADB89630 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 577
ID ADB90562 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 578
ID ADB77948 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 579
ID ADB39663 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 580
ID ADB75084 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 581
ID ADB47286 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 582
ID ADB86693 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 583
ID ADB77498 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 584
ID ADB34655 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
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PD 24-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 585
ID ADB35759 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 586
ID ADB34103 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 587
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 588
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 589
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 590
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 591
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 592
ID ADC40445 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 593
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 594
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 595
ID ADC29624 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 596
ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 597
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 598
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 599
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 600
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 601
ID AAE38826 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US200307657-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 602
ID ADC50579 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 7; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 603				
ID	ADCC7126 standard; protein; 310 AA.			
ID	Novel human secreted and transmembrane protein PRO1868.			
PN	US2003092107-A1.			
PD	15-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 604				
ID	ADCC6105 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein PRO1868.			
PN	US2003092105-A1.			
PD	15-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 605				
ID	ADCC3112 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087365-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 606				
ID	ADCC7466 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID558.			
PN	US2003087366-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 607				
ID	ADCC6657 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein PRO1868.			
PN	US2003087367-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 608				
ID	ADCC1132 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein PRO1868.			
PN	US2003087361-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 609				
ID	ADCC6559 standard; protein; 310 AA.			
DE	Human PRO polypeptide #269.			
PN	US2003087362-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 610				
ID	ADCC4757 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087363-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 611				
ID	ADCC3718 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087364-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 612				
ID	ADCC3718 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087364-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 613				
ID	ADCC3718 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087364-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 614				
ID	ADCC3718 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087364-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	27.5%;	Score 424;	DB 7;	Length 310;
Best Local Similarity	32.8%;	Pred. No. 7.5e-23;		
RESULT 615				
ID	ADCC3718 standard; protein; 310 AA.			
DE	Novel human secreted and transmembrane protein Seq ID538.			
PN	US2003087364-A1.			
PD	0			

Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	
RESULT 612			
ID	ADCS9241 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein Seq ID538.		
PN	US2003087359-A1.		
PD	08-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 613			
ID	ADCS6119 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein Seq ID538.		
PN	US2003087360-A1.		
PD	08-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 614			
ID	ADCS6689 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein Seq ID538.		
PN	US2003087346-A1.		
PD	08-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 615			
ID	ADCI2667 standard; protein; 310 AA.		
DE	Human secreted/transmembrane protein, #65.		
PN	US2003082541-A1.		
PD	01-MAY-2003		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 616			
ID	ADCT4383 standard; protein; 310 AA.		
DE	Human secreted protein - SEQ ID 1046.		
PN	WO2003038063-A2.		
PD	08-MAY-2003.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 617			
ID	ADCT74606 standard; protein; 310 AA.		
DE	Human secreted protein - SEQ ID 1239.		
PN	WO2003038063-A2.		
PD	08-MAY-2003.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 618			
ID	ADCT74607 standard; protein; 310 AA.		
DE	Human secreted protein - SEQ ID 1240.		
PN	WO2003038063-A2.		
PD	08-MAY-2003.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 619			
ID	ADDO3363 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein PRO1868.		
PN	US2003092104-A1.		
PD	15-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 620			
ID	ADCG0355 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein PRO1868.		
PN	US2003087348-A1.		
PD	08-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 621			
ID	ADCG0355 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein PRO1868.		
PN	US2003087348-A1.		
PD	08-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;
RESULT 622			
ID	ADCG0355 standard; protein; 310 AA.		
DE	Novel human secreted and transmembrane protein PRO1868.		
PN	US2003087348-A1.		
PD	08-MAY-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	27.5%;	Score 424;	DB 7;
Beef Local Similarity	32.8%;	Pred. No. 7.5e-23;	Length 310;

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RESULT 621
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 622
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 623
ID ADD10192 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 624
ID ADD04767 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 625
ID AD80723 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 626
ID ADD11330 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 627
ID AD10551 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 628
ID ADC4811 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 629
ID ADD05222 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 630
ID ADD37304 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 631
ID AD11511 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 632
ID ADD09640 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 633
ID ADD04228 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 634
ID ADD03804 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 635
ID ADD41353 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 636
ID ADD52492 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 637
ID ADD53232 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 638
ID ADD53784 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 639
ID ADD37304 standard; protein; 310 AA.
```

DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 640
ID ADD51940 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 641
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 642
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 643
ID ADD38009 standard; protein; 310 AA.
DE Human secreted protein #192.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 644
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 645
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 646
ID ADD5435 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 647
ID ADD92672 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 648
ID ADD91568 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 649
ID ADE04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 650
ID ADD32479 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 651
ID ADE22411 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 652
ID ADD79635 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 653
ID ADE42171 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 654
ID ADE17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 655
ID ADD92120 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 656
ID ADD33583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 657
ID ADE34135 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194791-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 658
ID ADD80187 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 659
ID ADD93234 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 660
ID ADE19644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 661
ID ADE35056 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US200307583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 662
ID ADE19092 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 663
ID ADE43288 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 664
ID ADE96077 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 665
ID ADE22963 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 666
ID ADD79081 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 667
ID ADE33031 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 668
ID ADE42723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 669
ID ADE80739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 670
ID ADE89767 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 671
ID ADE41051 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 672
ID ADE04850 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 673
ID ADE92979 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 674
ID ADE21688 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 675
ID ADE33329 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
ID ADF97664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 677
ID ADG80728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 678
ID ADG80176 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 679
ID ADH62558 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 680
ID ADH59539 standard; protein; 310 AA.
DE Human secreted/cranmembrane protein, #65.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 681
ID ADH55468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 682
ID ADH56020 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 683
ID ADI38318 standard; protein; 310 AA.
DE Human secreted/cranmembrane protein, #65.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 684

ID ADI64239 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 685
ID ADI65188 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 686
ID ADI63687 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 687
ID ADH82101 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 688
ID ADH81549 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 689
ID ADJ58518 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 690
ID ADJ26586 standard; protein; 310 AA.
DE Human secreted/cranmembrane protein, #65.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 691
ID ADM82718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 692
ID ADN16117 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 693
ID ADN16746 standard; protein; 310 AA.

DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 694
ID ADN15565 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 695
ID ADN15013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 696
ID ADG91275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 697
ID ADE79501 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 698
ID ADD76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 699
ID ADD88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 700
ID ADD86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 701
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 702
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 703
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 704
ID ADE41512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 705
ID ADE23515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 706
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 707
ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 708
ID ADD87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 709
ID ADE89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 710
ID ADE74136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 711
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 712
ID ADE88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 713
ID ADE99690 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 714
ID ADE94869 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 715
ID ADE91280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 716
ID ADE95421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 717
ID ADE93531 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 718
ID ADE95112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 719
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 720
ID ADE92427 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 721
ID ADE90728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 722
ID ADE91875 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 723
ID ADE99236 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 724
ID ADE40706 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 725
ID ADE74100 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 726
ID ADE02454 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 727
ID ADE22240 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 728
ID ADE020310 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
Query Match
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

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RESULT 729
ID ADF98216 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 730
ID ADG24433 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 731
ID ADF98787 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 732
ID ADG03618 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 733
ID ADF99339 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 734
ID ADG16924 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 735
ID ADG05383 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 736
ID ADG19650 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 737
ID ADP73676 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 738
ID ADG07920 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 739
ID ADG08544 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 740
ID ADG15714 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 741
ID ADF97112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 742
ID ADG06297 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 743
ID ADG23881 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 744
ID ADG04170 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 745
ID ADG35071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 746
ID ADG07368 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
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DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 748
ID ADG55415 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 749
ID ADG61079 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 750
ID ADG62183 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 751
ID ADG92519 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 752
ID ADG82384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 753
ID ADG57623 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 754
ID ADG57071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 755
ID ADG55967 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 756
ID ADG58727 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.

PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 757
ID ADG71093 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 758
ID ADG92946 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 759
ID ADG58175 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 760
ID ADG53759 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 761
ID ADG71645 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 762
ID ADG81832 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 763
ID ADH30794 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 764
ID ADH12161 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 765
ID ADG52583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207414-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 766
ID AD554311 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 767
ID ADG81280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 768
ID ADG56519 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 769
ID ADH12785 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 770
ID ADG61631 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 771
ID ADH28718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003202331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 772
ID ADG54863 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 773
ID ADG55993 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 774
ID ADH20735 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 775
ID ADH43695 standard; protein; 310 AA.
DE Human PRO polypeptide #131.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 776
ID ADH07590 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 777
ID ADH60135 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 778
ID ADH07163 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 779
ID ADH18137 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 780
ID ADH18905 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 781
ID ADI65625 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 782
ID ADH37884 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.

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PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 783
ID ADG10070 standard; protein: 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 784
ID ADH97684 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 785
ID ADI1541 standard; protein: 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 786
ID ADG09418 standard; protein: 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 787
ID ADI66052 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 788
ID ADI10341 standard; protein: 310 AA.
DE Human PRO1868 protein from DNA7624-2515 clone.
PN US2003228664-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 789
ID ADI14673 standard; protein: 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 790
ID ADH60795 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODDOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 791
ID ADI1468 standard; protein: 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 792
ID ADJ9852 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 793
ID ADL09045 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 794
ID ADI47177 standard; protein: 310 AA.
DE Human JAM-2 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 795
ID ADM25386 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 796
ID ADJ63749 standard; protein: 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 797
ID ADM30136 standard; protein: 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 798
ID ADL78563 standard; protein: 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2045.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 27.5%; Score 424; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 799
ID ADL78564 standard; protein: 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2046.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
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PA (HASE/) HASELTINE W A. 27.5%; Score 424; DB 8; Length 310;
 Query Match 32.8%; Pred. No. 7.5e-23;
 RESULT 800
 ID AD178565 standard; protein; 310 AA.
 DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2047.
 PN US2004010334-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (HASE/) HASELTINE W A.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 801
 ID ADJ77644 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2004038336-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 802
 ID ADR83040 standard; protein; 310 AA.
 DE Human PRO polypeptide #131.
 PN US2004043927-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 803
 ID ADJ65766 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2004038335-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 804
 ID ADJ30812 standard; protein; 310 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 2845.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 805
 ID ADJ32018 standard; protein; 310 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 4051.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 806
 ID ADM27902 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2004048333-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 807
 ID ADM42626 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2004058424-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 808
 ID ADO06458 standard; protein; 310 AA.
 DE Human PRO polypeptide #60.
 PN US6686451-B1.
 PD 03-FEB-2004.

PA (GETH) GENENTECH INC. 27.5%; Score 424; DB 8; Length 310;
 Query Match 32.8%; Pred. No. 7.5e-23;
 RESULT 809
 ID ADN35310 standard; protein; 310 AA.
 DE Human PRO1868 protein.
 PN WO2004031105-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 810
 ID ADM28488 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US200407064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 811
 ID ADPE9027 standard; protein; 310 AA.
 DE Human NOV2b protein SEQ ID NO:22.
 PN WO2004055158-A2.
 PD 01-JUL-2004.
 PA (CURA-) CURAGEN CORP.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 812
 ID ADPE9025 standard; protein; 310 AA.
 DE Human NOV2a protein SEQ ID NO:20.
 PN WO2004055158-A2.
 PD 01-JUL-2004.
 PA (CURA-) CURAGEN CORP.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 813
 ID ADPE9033 standard; protein; 310 AA.
 DE Human NOV2e protein SEQ ID NO:28.
 PN WO2004055158-A2.
 PD 01-JUL-2004.
 PA (CURA-) CURAGEN CORP.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 814
 ID ADPE9035 standard; protein; 310 AA.
 DE Human NOV2f protein SEQ ID NO:30.
 PN WO2004055158-A2.
 PD 01-JUL-2004.
 PA (CURA-) CURAGEN CORP.
 Query Match 27.5%; Score 424; DB 8; Length 310;
 Best Local Similarity 32.8%; Pred. No. 7.5e-23;
 RESULT 815
 ID ADR18219 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSSTEIN D.
 PA (DESN/) DESNOTERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 817
ID ADI95970 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 818
ID ADI96522 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 819
ID ADS74858 standard; protein; 310 AA.
DE Human secreted/transmembrane protein #65.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FILVAROFF E.
PA (FRONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 820
ID ADS32474 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 821
ID AAB38333 standard; protein; 311 AA.
DE Human PRO polypeptide #269.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 822
ID ADT03458 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 823
ID ADT03509 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 824
ID ABA38133 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 825
ID ABB14255 standard; protein; 310 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 538.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BEREZINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FLIV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
Best Local Similarity 27.5%; Score 424; DB 8; Length 310;
Pred. No. 7.5e-23;
RESULT 826
ID AAB38383 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO20061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 3; Length 311;
Pred. No. 7.5e-23;
RESULT 827
ID AAB38384 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO20061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 27.5%; Score 424; DB 3; Length 311;
Pred. No. 7.5e-23;
RESULT 828
ID AAB38333 standard; protein; 311 AA.

DE Human secreted protein encoded by gene 13 clone HAFSA79.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.5%; Score 424; DB 3; Length 311;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 829
ID ABR41902 standard; protein; 329 AA.
DE Human ovarian antigen HISAf60, SEQ ID NO:3034.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.5%; Score 424; DB 5; Length 329;
Best Local Similarity 32.8%; Pred. No. 8e-23;
RESULT 830
ID AAB80431 standard; peptide; 339 AA.
DE Gene #13 associated peptide #1.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 27.5%; Score 424; DB 4; Length 339;
Best Local Similarity 32.8%; Pred. No. 8.3e-23;
RESULT 831
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN WO200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 27.1%; Score 419; DB 3; Length 310;
Best Local Similarity 32.8%; Pred. No. 1.7e-22;
RESULT 832
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (hujam3) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 27.1%; Score 419; DB 8; Length 310;
Best Local Similarity 32.8%; Pred. No. 1.7e-22;
RESULT 833
ID AAM23693 standard; protein; 303 AA.
DE Human EST encoded protein SEQ ID NO: 1218.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 26.9%; Score 415.5; DB 4; Length 303;
Best Local Similarity 34.4%; Pred. No. 3e-22;
RESULT 834
ID AAB27278 standard; protein; 310 AA.
DE Murine confuency regulated adhesion molecule 1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 26.9%; Score 415; DB 3; Length 310;
Best Local Similarity 33.8%; Pred. No. 3.4e-22;
RESULT 835
ID AAB27272 standard; protein; 310 AA.
DE Human confuency regulated adhesion molecule 1 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 26.9%; Score 415; DB 3; Length 310;
Best Local Similarity 33.8%; Pred. No. 3.4e-22;
RESULT 836
ID ADK40850 standard; peptide; 76 AA.
DE Human F11-adhesion molecule (FAM) conserved region #1.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UNY) UNIV NEW YORK STATE RES FOUND.
Query Match 26.7%; Score 412; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
RESULT 837
ID ADU66690 standard; protein; 76 AA.
DE Human FAM C2-type Ig domain #1.

PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
Query Match 26.7%; Score 412; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
RESULT 838
ID AAB39254 standard; protein; 285 AA.
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.7%; Score 412; DB 3; Length 285;
Best Local Similarity 33.1%; Pred. No. 5.1e-22;
RESULT 839
ID ADK40852 standard; peptide; 76 AA.
DE Human F11-adhesion molecule (FAM) conserved region #2.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UNY) UNIV NEW YORK STATE RES FOUND.
Query Match 26.5%; Score 409; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
RESULT 840
ID ADU66692 standard; protein; 76 AA.
DE Human FAM C2-type Ig domain #2.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
Query Match 26.5%; Score 409; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
RESULT 841
ID AAY23324 standard; protein; 312 AA.
DE A33 related antigen PRO245.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 2; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 842
ID AAY08060 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 2; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 843
ID AAY13354 standard; protein; 312 AA.
DE Amino acid sequence of protein PRO245.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 2; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 844
ID AAB33421 standard; protein; 312 AA.
DE Human PRO245 protein UNQ219 SEQ ID NO:36.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 3; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 845
ID AAY70668 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200015787-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 3; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 846
ID AAB24401 standard; protein; 312 AA.

DE Human PRO245 protein sequence SEQ ID NO:67.
PN W0200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 3; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 847
ID ADC78384 standard; protein; 312 AA.
DE Human PRO245 protein.
PN W0200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 3; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 848
ID AAB80222 standard; protein; 312 AA.
DE Human PRO245 protein.
PN W0200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 4; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 849
ID AAU00821 standard; protein; 312 AA.
DE Human immune response protein PRO245 (UNQ219).
PN W0200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 4; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 850
ID AAU12339 standard; protein; 312 AA.
DE Human PRO245 polypeptide sequence.
PN W0200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 4; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 851
ID AAB53081 standard; protein; 312 AA.
DE Human angiogenesis-associated protein PRO245, SEQ ID NO:91.
PN W0200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 4; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 852
ID ABU71600 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 853
ID ABO17783 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 854
ID ABU71455 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 855
ID ABU81037 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 856
ID ABU71901 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 857
ID ABO01784 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 858
ID ABU66737 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 859
ID ABU54357 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 860
ID ABO47372 standard; protein; 312 AA.
DE Human secreted/transmembrane polypeptide PRO245.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 861
ID ABU59818 standard; protein; 312 AA.
DE Novel secreted and transmembrane protein PRO245.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 862
ID ABO25008 standard; protein; 312 AA.
DE Human secreted/transmembrane protein (PRO) #168.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 863
ID ABU64509 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 864
ID ABU67355 standard; protein; 312 AA.
DE Human secreted protein PRO245.
PN US2003023054-A1.

PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 865
ID ABO14875 standard; protein; 312 AA.
DE Human secreted / transmembrane polypeptide PRO245.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 866
ID ABO07738 standard; protein; 312 AA.
DE Human A-33 related antigen PRO245.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 867
ID ABO67013 standard; protein; 312 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 336.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 868
ID ABO69632 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 869
ID ABO14814 standard; protein; 312 AA.
DE Human secreted / transmembrane polypeptide PRO245.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 870
ID ADA45855 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 871
ID ADA76286 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 872
ID ADB29269 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 873
ID ADA18936 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 874
ID ADA61559 standard; protein; 312 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 875
ID ADB19344 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 876
ID ADB27885 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 877
ID ADA86364 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 878
ID ADA15928 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 879
ID ADA47714 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 880
ID ADA18125 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 881
ID ABO32766 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 882
ID ADA67509 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 883
ID ADB30516 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 884
ID ADA85812 standard; protein: 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 885
ID ADA97024 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 886
ID ADA79328 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 887
ID ADA87467 standard; protein: 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 888
ID ADB16669 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 889
ID ABO34626 standard; protein: 312 AA.
DE Human PRO polypeptide #11.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 890
ID ADA16100 standard; protein: 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 891
ID ADA91761 standard; protein: 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;

Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 892
ID ADB14824 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 893
ID ADB18785 standard; protein: 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 894
ID ADA94000 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 895
ID ADB19696 standard; protein: 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 896
ID ADB13208 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 897
ID ABO43316 standard; protein: 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 898
ID ADA74462 standard; protein: 312 AA.
DE Human PRO polypeptide #168.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 899
ID ADA42245 standard; protein: 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;
RESULT 900
ID ADB24695 standard; protein: 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2% Score 404; DB 6; Length 312;
Best Local Similarity 35.2% Pred. No. 2.2e-21;

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RESULT 901
ID ADA82219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 902
ID ADA75182 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 903
ID ADA85260 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 904
ID ADA84708 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 905
ID ABO17504 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 906
ID ADB24964 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 907
ID ADA80492 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 908
ID ADA75734 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 909
ID ADA46959 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 910
ID ADB26229 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 911
ID ADA93431 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 912
ID ADB26781 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 913
ID ADB31068 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 914
ID ADA60996 standard; protein; 312 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 915
ID ADB24143 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 916
ID ADA96472 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 917
ID ADA81044 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 918
ID ADA95920 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 919
ID ADB26229 standard; protein; 312 AA.
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DE Human PRO polypeptide #168.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 920
ID ADB2114 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 921
ID ADA77493 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 922
ID ADB18233 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 923
ID ADB6616 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 924
ID ADA16524 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 925
ID ADA12953 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 926
ID ADA41621 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 927
ID ADA88019 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 928
ID ADA46407 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 929
ID ADA17168 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 930
ID ADA42671 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 931
ID ADB28437 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 932
ID ADB28989 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 933
ID ADA76941 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 934
ID ADA88571 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 935
ID ADA97576 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 936
ID ADB27333 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003022339-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 937
ID ADB22266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087344-A1.
PD 08-MAY-2003.

Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 938				
ID ABO17565 standard; protein; 312 AA.				
DE Human PRO polypeptide #11.				
PN US2003064923-A1.				
PD 03-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 939				
ID ADA66957 standard; protein; 312 AA.				
DE Human PRO polypeptide #168.				
PN US2003068793-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 940				
ID ADA82818 standard; protein; 312 AA.				
DE Human PRO polypeptide #168.				
PN US2003077711-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 941				
ID ADA23591 standard; protein; 312 AA.				
DE Human PRO polypeptide SEQ ID NO 336.				
PN US2003077712-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 942				
ID ADA92313 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003082712-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 943				
ID ADA15376 standard; protein; 312 AA.				
DE Human PRO polypeptide #168.				
PN US2003087352-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 944				
ID ADA38628 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US200308276-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 945				
ID ADA38076 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003087347-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 946				
ID ADA66548 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003082889-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 947				
ID ADA66548 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003082889-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 948				
ID ADA66548 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003082889-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 949				
ID ADA66548 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003082889-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26.2%;	Score 404;	DB 7;	Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 950				
ID ADA66548 standard; protein; 312 AA.				
DE Novel human secreted and transmembrane protein PRO245.				
PN US2003082889-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	26			

Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 947		
ID	ADB89628 standard; protein; 312 AA.	
DE	Human PRO polypeptide #168.	
PN	US2003082698-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 948		
ID	ADB90360 standard; protein; 312 AA.	
DE	Human PRO polypeptide #168.	
PN	US2003082762-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 949		
ID	ADB77590 standard; protein; 312 AA.	
DE	Human secreted/transmembrane protein, #13.	
PN	US2003077654-A1.	
PD	24-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 950		
ID	ADB39461 standard; protein; 312 AA.	
DE	Novel human secreted and transmembrane protein PRO245.	
PN	US2003082764-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 951		
ID	ADB74726 standard; protein; 312 AA.	
DE	Human secreted/transmembrane protein, #13.	
PN	US2003082542-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 952		
ID	ADB747084 standard; protein; 312 AA.	
DE	Novel human secreted and transmembrane protein PRO245.	
PN	US2003082687-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 953		
ID	ADB86691 standard; protein; 312 AA.	
DE	Human PRO polypeptide #168.	
PN	US2003082697-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 954		
ID	ADB77296 standard; protein; 312 AA.	
DE	Novel human secreted and transmembrane protein PRO245.	
PN	US2003082696-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;
RESULT 955		
ID	ADB34453 standard; protein; 312 AA.	
DE	Human PRO polypeptide SPQ ID NO 336.	
PN	US2003077717-A1.	
PD	24-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	26.2%;	Score 404; DB 7; Length 312;
Best Local Similarity	35.2%;	Pred. No. 2.2e-21;

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RESULT 956
ID ADB35557 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 957
ID ADB33901 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 958
ID ADB35005 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 959
ID ADB36109 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 960
ID ADB46504 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 961
ID ADC28372 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 962
ID ADC39572 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 963
ID ADC40086 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 964
ID ADC18914 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 965
ID ADC59903 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 966
ID ADC29265 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 967
ID ADC28796 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 968
ID ADC40681 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 969
ID ADC19338 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 970
ID ADC33786 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 971
ID ADC12856 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 972
ID ADC50377 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 973
ID ADC71924 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 974
ID ADC59903 standard; protein; 312 AA.
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DE Novel human secreted and transmembrane protein PRO245.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 975
ID ADC52910 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 976
ID ADC57264 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 977
ID ADC60455 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 978
ID ADC50930 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 979
ID ADC65457 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 980
ID ADC54555 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 981
ID ADC53516 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 982
ID ADC59039 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 983
ID ADC55917 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.

PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 984
ID ADC58487 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 985
ID ADC12308 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 986
ID ADD03161 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 987
ID ADC90153 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 988
ID ADC69572 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 989
ID ADC48461 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 990
ID ADD09990 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 991
ID ADD04565 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 992
ID ADC80521 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092103-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 993
ID ADD11028 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 994
ID ADC47909 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 995
ID ADD04863 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 996
ID ADC79969 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 997
ID ADD09438 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 998
ID ADD03869 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 999
ID ADD03445 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1000
ID ADD41151 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1001
ID ADD52290 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1002
ID ADD53030 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1003
ID ADD53582 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1004
ID ADD51738 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1005
ID ADD02537 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1006
ID ADD01971 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1007
ID ADD54153 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1008
ID ADD92470 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1009
ID ADD91366 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1010
ID ADE03980 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1011
ID ADE32277 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1012
ID ADE22209 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1013
ID ADE79453 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1014
ID ADE41969 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1015
ID ADE17786 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1016
ID ADE91918 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1017
ID ADE33381 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1018
ID ADE33933 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1019
ID ADE79985 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;

Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1020
ID ADE93022 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1021
ID ADE19442 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1022
ID ADE34697 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US200307583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1023
ID ADE18890 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1024
ID ADE43086 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1025
ID ADE95875 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1026
ID ADE22761 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1027
ID ADE78879 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1028
ID ADE32829 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          26.2%  Score 404; DB 7; Length 312;
Best Local Similarity 35.2%  Pred. No. 2.2e-21;
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RESULT 1029
ID AD642521 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1030
ID ADD80537 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1031
ID AD89565 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1032
ID AD840849 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1033
ID ADE04648 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1034
ID ADE92777 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1035
ID AOG21486 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1036
ID AOG23127 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1037
ID ADE97462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1038
ID ADG80526 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1039
ID ADG79974 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1040
ID ADH62536 standard; protein; 312 AA.
DE Human PRO245 protein encoded by DNA35638 cDNA.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1041
ID ADH59180 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1042
ID ADH55266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1043
ID ADH55818 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1044
ID ADI37959 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1045
ID ADI64986 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1046
ID ADH81899 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207388-A1.
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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1047
ID AD81347 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US200307377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1048
ID AD32627 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1049
ID AD82516 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1050
ID AD15915 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1051
ID AD16544 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1052
ID AD11563 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1053
ID AD11481 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1054
ID AD16407 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1055
ID AD163485 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1056
ID AD81073 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1057
ID AD879142 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1058
ID AD76521 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1059
ID AD87885 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1060
ID AD86289 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1061
ID AD87956 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1062
ID AD875737 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1063
ID AD873242 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1064
ID AD82313 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1065
ID ADE23865 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1066
ID ADE24508 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1067
ID ADD87333 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1068
ID ADE89199 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1069
ID ADE73777 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1070
ID ADE18338 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1071
ID ADE88647 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1072
ID ADE99331 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1073
ID ADE94667 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1074
ID ADE91078 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1075
ID ADE95219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1076
ID ADE93329 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1077
ID ADF34910 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1078
ID ADE98450 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1079
ID ADE92225 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1080
ID ADE90526 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1081
ID ADE91673 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1082
ID ADE98877 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
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RESULT 1083	ID	ADG40347	standard; protein; 312 AA.		
DE	ID	Human secreted/transmembrane protein, #13.			
	PN	US2003225253-A1.			
	PD	04-DEC-2003.			
	PA	(DESN/) DESNOYERS L.			
PA	(GDDP/) GODDARD A.				
	PA	(GDDP/) GODOWSKI P J.			
	PA	(GURN/) GURNER A L.			
	PA	(MATH/) MATHNEY J P.			
PA	(WILL/) WILLIAMS P M.				
	PA	(WOOD/) WOOD W I.			
	Query Match	26.2%;	Score 404; DB 8;	Length 312;	
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
RESULT 1084	ID	ADPF73741	standard; protein; 312 AA.		
DE	ID	Human secreted/transmembrane protein, #13.			
	PN	US2003180312-A1.			
	PD	25-SEP-2003.			
	PA	(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1085	ID	ADG02252	standard; protein; 312 AA.	
	DE	ID	Human PRO polypeptide #168.		
PN		US2003207352-A1.			
PD		06-NOV-2003.			
PA		(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1086	ID	ADG22038	standard; protein; 312 AA.	
	DE	ID	Novel human secreted and transmembrane protein PRO245.		
PN		US2003207360-A1.			
PD		06-NOV-2003.			
PA		(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1087	ID	ADG20108	standard; protein; 312 AA.	
	DE	ID	Human PRO polypeptide #168.		
PN		US2003207376-A1.			
PD		06-NOV-2003.			
PA		(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1088	ID	ADPF98014	standard; protein; 312 AA.	
	DE	ID	Human PRO polypeptide #168.		
PN		US2003207422-A1.			
PD		06-NOV-2003.			
PA		(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1089	ID	ADG24231	standard; protein; 312 AA.	
	DE	ID	Novel human secreted and transmembrane protein PRO245.		
PN		US2003207426-A1.			
PD		06-NOV-2003.			
PA		(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1090	ID	ADPF98585	standard; protein; 312 AA.	
	DE	ID	Human PRO polypeptide #168.		
PN		US2003208055-A1.			
PD		06-NOV-2003.			
PA		(GETH) GENENTECH INC.			
Query Match	26.2%;	Score 404; DB 8;	Length 312;		
	Best Local Similarity	35.2%;	Pred. No. 2.2e-21;		
	RESULT 1091	ID	ADG03416	standard; protein; 312 AA.	
	DE	ID	Human PRO polypeptide #168		

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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1101
ID ADG06095 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1102
ID ADG23679 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1103
ID ADG03968 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1104
ID ADG24869 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1105
ID ADG07166 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1106
ID ADG07718 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1107
ID ADG5513 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1108
ID ADG60877 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1109
ID ADG61981 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1110
ID ADG92160 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1111
ID ADG82182 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1112
ID ADG57421 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1113
ID ADG56869 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1114
ID ADG55765 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1115
ID ADG58525 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1116
ID ADG70891 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1117
ID ADG92587 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1118
ID ADG57973 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;


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Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1119
ID  ADG53557 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307415-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1120
ID  ADG71443 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US2003207421-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1121
ID  ADG81630 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US2003207805-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1122
ID  ADH30592 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US2003077723-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1123
ID  ADH1959 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307419-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1124
ID  ADG52381 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307414-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1125
ID  ADG54109 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307416-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1126
ID  ADG81078 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US2003194793-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1127
ID  ADG56317 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307366-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1128
ID  ADH12583 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307378-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1129
ID  ADG61429 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307429-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1130
ID  ADH28516 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US200302331-A1.
PD  30-JAN-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1131
ID  ADG54661 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307367-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1132
ID  ADG59701 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US200307369-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1133
ID  ADH20376 standard; protein; 312 AA.
DE  Human secreted/transmembrane protein. #13.
PN  US2004005553-A1.
PD  08-JAN-2004.
PA  (DESN/) DESNOYERS L.
PA  (GDD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MAT/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1134
ID  ADH07231 standard; protein; 312 AA.
DE  Human secreted/transmembrane protein. #13.
PN  US2004006211-A1.
PD  08-JAN-2004.
PA  (DESN/) DESNOYERS L.
PA  (GDD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MAT/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1135
ID  ADH59776 standard; protein; 312 AA.
DE  Human secreted/transmembrane protein. #13.
PN  US2003215804-A1.
PD  20-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match                26.2%  Score 404; DB 8; Length 312;
Best Local Similarity      35.2%  Pred. No. 2.2e-21;
RESULT 1136
ID  ADH06804 standard; protein; 312 AA.
DE  Human secreted/transmembrane protein. #13.
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PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1137
ID ADH81125 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1138
ID ADH18546 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003152939-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1139
ID ADH65266 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1140
ID ADH37529 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1141
ID ADH9733 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1142
ID ADH9733 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1143
ID ADH1539 standard; protein; 312 AA.
DE Novel human secreted and cranmembrane protein PRO245.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1144
ID ADG09216 standard; protein; 312 AA.
DE Novel human secreted and cranmembrane protein PRO245.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1145
ID ADH14671 standard; protein; 312 AA.
DE Novel human secreted and cranmembrane protein PRO245.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1146
ID ADH60436 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1147
ID ADH18266 standard; protein; 312 AA.
DE Novel human secreted and cranmembrane protein PRO245.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1148
ID ADH9493 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1149
ID ADH0686 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1150
ID ADM25031 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1151
ID ADH6347 standard; protein; 312 AA.
DE Novel human secreted and cranmembrane protein PRO245.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1152
ID ADM29777 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1153
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ID ADJ7442 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1154
ID ADJ65564 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1155
ID ADM27700 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1156
ID ADM42424 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1157
ID ADO06099 standard; protein; 312 AA.
DE Human PRO polypeptide #1.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1158
ID ADN35292 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1159
ID ADM28286 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1160
ID ADRI0951 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1161
ID ADRI7860 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (GONW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PRON/) PRONI N F.
PA (ROTM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1162
ID ADI95768 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200307659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1163
ID ADI96320 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1164
ID ADI65693 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein, #13.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1165
ID ADP94237 standard; protein; 312 AA.
DE Human PRO245 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      26.2%  Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%  Pred. No. 2.2e-21;
RESULT 1166
ID ADJ74499 standard; protein; 312 AA.
DE Human secreted/cranmembrane protein #13.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
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PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANT/) PANT J.
PA (PAON/) PAONT N F.
PA (ROYM/) ROY W A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1167
ID ADS32272 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH/) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1168
ID ADP03256 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH/) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1169
ID ADP03536 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH/) GENENTECH INC.
Query Match 26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1170
ID ADZ03307 standard; protein; 312 AA.
DE Human secreted/transmembrane PRO245 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH/) GENENTECH INC.
Query Match 26.2%; Score 404; DB 9; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1171
ID AEA37774 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH/) GENENTECH INC.
Query Match 26.2%; Score 404; DB 9; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1172
ID AEB14053 standard; protein; 312 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 336.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINT M.
PA (DEFO/) DEFOUR L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.

Query Match 26.2%; Score 404; DB 9; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1173
ID ADP56682 standard; protein; 323 AA.
DE Human junction adhesion molecule 2 splice variant (nuJAM2sv) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIT/) LILLY & CO ELI.
Query Match 26.2%; Score 404; DB 8; Length 323;
Best Local Similarity 35.2%; Pred. No. 2.3e-21;
RESULT 1174
ID AAB50904 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH/) GENENTECH INC.
Query Match 26.0%; Score 402; DB 4; Length 312;
Best Local Similarity 35.2%; Pred. No. 3.1e-21;
RESULT 1175
ID AAM41947 standard; protein; 222 AA.
DE Human polypeptide SEQ ID NO 6878.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.9%; Score 399.5; DB 4; Length 222;
Best Local Similarity 38.5%; Pred. No. 3.1e-21;
RESULT 1176
ID AAB70500 standard; protein; 215 AA.
DE Angiogenesis protein AAI1 protein sequence (Fig 8).
PN WO200111086-A2.
PD 15-FEB-2001.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 25.6%; Score 395.5; DB 4; Length 215;
Best Local Similarity 39.4%; Pred. No. 5.9e-21;
RESULT 1177
ID AAB27277 standard; protein; 213 AA.
DE Human confuency regulated adhesion molecule 2 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 25.4%; Score 392.5; DB 3; Length 213;
Best Local Similarity 39.7%; Pred. No. 9.8e-21;
RESULT 1178
ID AAB27273 standard; protein; 298 AA.
DE Human confuency regulated adhesion molecule 2 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 25.3%; Score 391; DB 3; Length 298;
Best Local Similarity 33.4%; Pred. No. 1.9e-20;
RESULT 1179
ID AAB27275 standard; protein; 298 AA.
DE Murine confuency regulated adhesion molecule 2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 25.3%; Score 391; DB 3; Length 298;
Best Local Similarity 33.4%; Pred. No. 1.9e-20;
RESULT 1180
ID ABB06037 standard; protein; 321 AA.
DE Human NS protein sequence SEQ ID NO:129.
PN WO200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match 25.2%; Score 389; DB 5; Length 321;
Best Local Similarity 33.2%; Pred. No. 2.8e-20;
RESULT 1181
ID ABG22341 standard; protein; 388 AA.
DE Novel human diagnostic protein #22332.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.1%; Score 387.5; DB 4; Length 388;

Best Local Similarity 34.2%; Pred. No. 4.6e-20;
RESULT 1182
ID ADP17957 standard; protein; 102 AA.
DE Murine junction adhesion molecule protein used to create novel VAPs.
PN EPI318195-A1.
PD 11-JUN-2003.
PA (CATCH-) CATCHMABS BV.
Query Match 23.8%; Score 367; DB 7; Length 102;
Best Local Similarity 66.0%; Pred. No. 3e-19;
RESULT 1183
ID ADO65675 standard; protein; 259 AA.
DE Novel human protein sequence #48.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.8%; Score 351.5; DB 8; Length 259;
Best Local Similarity 28.8%; Pred. No. 1.2e-17;
RESULT 1184
ID AAO30179 standard; protein; 235 AA.
DE Human novel splice variant of VEJAM (NOJAM).
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST-) GESTET SA.
Query Match 22.1%; Score 341.5; DB 6; Length 235;
Best Local Similarity 38.1%; Pred. No. 5.9e-17;
RESULT 1185
ID ADP66685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (huJAM3bv2) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (EULI-) LILLY & CO EULI.
Query Match 21.1%; Score 326.5; DB 8; Length 265;
Best Local Similarity 32.9%; Pred. No. 8.5e-16;
RESULT 1186
ID ADU06841 standard; protein; 265 AA.
DE Cell adhesion and extracellular matrix protein clone 7518734CD1.
PN WO2004094623-A2.
PD 04-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 21.1%; Score 326.5; DB 8; Length 265;
Best Local Similarity 32.9%; Pred. No. 8.5e-16;
RESULT 1187
ID ADP12431 standard; protein; 238 AA.
DE Human adhesion molecule JAM-2.
PN WO2003087128-A2.
PD 23-OCT-2003.
PA (RMPD-) RMP DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 21.0%; Score 325; DB 7; Length 238;
Best Local Similarity 33.1%; Pred. No. 9.7e-16;
RESULT 1188
ID ADG39449 standard; protein; 238 AA.
DE Human JAM-2 protein SEQ ID NO:18.
PN WO2003104400-A2.
PD 18-DEC-2003.
PA (RMPD-) RMP DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 21.0%; Score 325; DB 8; Length 238;
Best Local Similarity 33.1%; Pred. No. 9.7e-16;
RESULT 1189
ID ABG22401 standard; protein; 361 AA.
DE Novel human diagnostic protein #22392.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 20.4%; Score 315; DB 4; Length 361;
Best Local Similarity 33.0%; Pred. No. 8.5e-15;
RESULT 1190
ID AAU18007 standard; protein; 105 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 152.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 20.1%; Score 310.5; DB 4; Length 105;
Best Local Similarity 66.7%; Pred. No. 4.3e-15;
RESULT 1191
ID AAM96332 standard; protein; 105 AA.
DE Human reproductive system related antigen SEQ ID NO: 4990.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.1%; Score 310.5; DB 4; Length 105;
Best Local Similarity 66.7%; Pred. No. 4.3e-15;
RESULT 1192
ID ABB10436 standard; protein; 105 AA.
DE Human cDNA SEQ ID NO: 744.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.1%; Score 310.5; DB 4; Length 105;
Best Local Similarity 66.7%; Pred. No. 4.3e-15;
RESULT 1193
ID ABP67023 standard; protein; 105 AA.
DE Human polypeptide SEQ ID NO 744.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 20.1%; Score 310.5; DB 5; Length 105;
Best Local Similarity 66.7%; Pred. No. 4.3e-15;
RESULT 1194
ID ADB11631 standard; protein; 105 AA.
DE Human novel protein SEQ ID NO 152.
PN US200307606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.1%; Score 310.5; DB 7; Length 105;
Best Local Similarity 66.7%; Pred. No. 4.3e-15;
RESULT 1195
ID ADP69098 standard; protein; 206 AA.
DE Human NOV2a mature extracellular domain protein SEQ ID NO:68.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 19.8%; Score 305; DB 8; Length 206;
Best Local Similarity 34.0%; Pred. No. 2.4e-14;
RESULT 1196
ID ADP69031 standard; protein; 206 AA.
DE Human NOV2d protein SEQ ID NO:26.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 19.8%; Score 305; DB 8; Length 206;
Best Local Similarity 34.0%; Pred. No. 2.4e-14;
RESULT 1197
ID ADP69029 standard; protein; 206 AA.
DE Human NOV2c protein SEQ ID NO:24.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 19.8%; Score 305; DB 8; Length 206;
Best Local Similarity 34.0%; Pred. No. 2.4e-14;
RESULT 1198
ID AAW14158 standard; protein; 318 AA.
DE Mouse A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 18.4%; Score 284.5; DB 2; Length 318;
Best Local Similarity 29.5%; Pred. No. 1.3e-12;
RESULT 1199
ID ADP66684 standard; protein; 229 AA.
DE Human junction adhesion molecule 3 splice variant 1 (huJAM3bv1) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.

RESULT 1216
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 17.4%; Score 269; DB 2; Length 268;
PRED. NO. 1.4e-11;
RESULT 1217
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 17.4%; Score 269; DB 7; Length 268;
PRED. NO. 1.4e-11;
RESULT 1218
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 17.4%; Score 269; DB 2; Length 270;
PRED. NO. 1.4e-11;
RESULT 1219
ID AAO11807 standard; protein; 134 AA.
DE Human polypeptide SEQ ID NO 25699.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 15.6%; Score 240.5; DB 4; Length 134;
PRED. NO. 7.6e-10;
RESULT 1220
ID ABG04645 standard; protein; 291 AA.
DE Novel human diagnostic protein #4636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 15.1%; Score 233.5; DB 4; Length 291;
PRED. NO. 6.1e-09;
RESULT 1221
ID ABM84859 standard; protein; 344 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:5108.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 15.1%; Score 233.5; DB 8; Length 344;
PRED. NO. 7.4e-09;
RESULT 1222
ID ABG12109 standard; protein; 404 AA.
DE Novel human diagnostic protein #12100.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 15.1%; Score 233.5; DB 4; Length 404;
PRED. NO. 8.9e-09;
RESULT 1223
ID AAY87251 standard; protein; 327 AA.
DE Human signal peptide containing protein HSP-28 SEQ ID NO:28.
PN WO200006010-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 3; Length 327;
PRED. NO. 9e-09;
RESULT 1224
ID AAY94857 standard; protein; 327 AA.
DE Human protein clone HP10568.

PN WO200005367-A2.
PD 03-FEB-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 3; Length 327;
PRED. NO. 9e-09;
RESULT 1225
ID AAB08903 standard; protein; 327 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:60.
PN WO20017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 3; Length 327;
PRED. NO. 9e-09;
RESULT 1226
ID AAY97585 standard; protein; 327 AA.
DE Human secreted protein PRO7154.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 4; Length 327;
PRED. NO. 9e-09;
RESULT 1227
ID ABB90354 standard; protein; 327 AA.
DE Human polypeptide SEQ ID NO 2730.
PN WO200150304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 5; Length 327;
PRED. NO. 9e-09;
RESULT 1228
ID AAU83709 standard; protein; 327 AA.
DE Human PRO protein, Seq ID No 236.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 5; Length 327;
PRED. NO. 9e-09;
RESULT 1229
ID ADJ31976 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 5; Length 327;
PRED. NO. 9e-09;
RESULT 1230
ID ABU80856 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 6; Length 327;
PRED. NO. 9e-09;
RESULT 1231
ID ABO33822 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 6; Length 327;
PRED. NO. 9e-09;
RESULT 1232
ID ABU82165 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.0%; Score 232; DB 6; Length 327;
PRED. NO. 9e-09;
RESULT 1233
ID AB723345 standard; protein; 327 AA.
DE Human PRO7154 protein.

PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 6; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1234
ID ABB72473 standard; protein; 327 AA.
DE Human PRO7154 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 6; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1235
ID ABO34368 standard; protein; 327 AA.
DE Human secreted/transmembrane polypeptide PRO 7154.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 6; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1236
ID ABB72175 standard; protein; 327 AA.
DE Human membrane bound receptor/protein PRO7154 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1237
ID ABB83726 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1238
ID ABB80832 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1239
ID ABB73373 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1240
ID ABB78455 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1241
ID ABB85103 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1242
ID ABB78209 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003092886-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1243
ID ABB87275 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1244
ID ABB84857 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1245
ID ABB83972 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1246
ID ABB73127 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1247
ID ADC36965 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1248
ID ADC21955 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1249
ID ADC49986 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1250
ID ADC49185 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 7; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1251
ID ADC49702 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088071-A1.
PD 08-MAY-2003.

PA	(GETH) GENENTECH INC.	15.0%;	Score 232;	DB 7;	Length 327;
Query Match					
Best Local Similarity	29.4%;	Pred.	No.	9e-09;	
RESULT 1252					
ID	ADDC47563 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003088072-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1253					
ID	ADDC47308 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003105288-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1254					
ID	ADCF78183 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003096972-A1.				
PD	22-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1255					
ID	ADD06418 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003073816-A1.				
PD	17-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1256					
ID	ADCF77937 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003088066-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1257					
ID	ADD050900 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003105291-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1258					
ID	ADD51146 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003105290-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1259					
ID	ADD50627 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003096971-A1.				
PD	22-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1260					
ID	ADD50381 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003096970-A1.				
PD	22-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1261					
ID	ADD51392 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003105289-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 7;	Length 327;	
RESULT 1262					
ID	ADDC68939 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003092888-A1.				
PD	15-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					
Best Local Similarity	15.0%;	Score 232;	DB 8;	Length 327;	
RESULT 1263					
ID	ADBE21110 standard; protein; 327 AA.				
DE	Novel human secreted and transmembrane protein PRO7154.				
PN	US2003100735-A1.				
PD	29-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match					

Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1270
ID ADE39161 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1271
ID ADE05708 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1272
ID ADD73693 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1273
ID ADD76533 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1274
ID ADE21356 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1275
ID ADD77471 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1276
ID ADE20618 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1277
ID ADD75683 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1278
ID ADD74199 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;

RESULT 1279
ID ADD74445 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1280
ID ADD76175 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1281
ID ADD85667 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1282
ID ADE05216 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1283
ID ADD75429 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1284
ID ADD76973 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1285
ID ADD86741 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1286
ID ADD78209 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1287
ID ADD77717 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1288
ID ADD77717 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;

ID ADD77963 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1289
ID ADD85421 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1290
ID ADD73953 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1291
ID ADD74691 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1292
ID ADD77219 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1293
ID ADD85913 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1294
ID ADE05462 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1295
ID ADD74937 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1296
ID ADG05749 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096559-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1297
ID ADG27303 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003096562-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1298
ID ADG11366 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096567-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1299
ID ADG12145 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096563-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1300
ID ADP94702 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096564-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1301
ID ADG06798 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003096566-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1302
ID ADH39142 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096565-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1303
ID ADG34232 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1304
ID ADI33702 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003096560-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1305
ID ADH69796 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
RESULT 1306
ID ADI29957 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.

PN US2003096961-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 15.0%; Score 232; DB 8; Length 327;
 Best Local Similarity 29.4%; Pred. No. 9e-09;
 RESULT 1307
 ID ADM27354 standard; protein; 327 AA.
 DE Novel human secreted and transmembrane protein PRO7154.
 PN US2006044179-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 15.0%; Score 232; DB 8; Length 327;
 Best Local Similarity 29.4%; Pred. No. 9e-09;
 RESULT 1308
 ID ADK66712 standard; protein; 327 AA.
 PN US2004044180-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 15.0%; Score 232; DB 8; Length 327;
 Best Local Similarity 29.4%; Pred. No. 9e-09;
 RESULT 1309
 ID AAB53307 standard; protein; 365 AA.
 DE Human colon cancer antigen protein sequence SEQ ID NO:847.
 PN WO200055351-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.0%; Score 232; DB 3; Length 365;
 Best Local Similarity 29.4%; Pred. No. 1e-08;
 RESULT 1310
 ID AAG75613 standard; protein; 365 AA.
 DE Human colon cancer antigen protein SEQ ID NO:6377.
 PN WO200122820-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.0%; Score 232; DB 4; Length 365;
 Best Local Similarity 29.4%; Pred. No. 1e-08;
 RESULT 1311
 ID ADP83097 standard; protein; 326 AA.
 DE Human corticol chymocyte receptor CTXL, overexpressed in cancer.
 PN WO2003100000-A2.
 PD 04-DEC-2003.
 PA (TULA-) TULARIK INC.
 Query Match 14.8%; Score 229; DB 8; Length 326;
 Best Local Similarity 28.8%; Pred. No. 1.5e-08;
 RESULT 1312
 ID ADK40847 standard; peptide; 42 AA.
 DE Human platelet F11-adhesion molecule (FAM), peptide #1.
 PN US6699688-B1.
 PD 02-MAR-2004.
 PA (UTNY) UNIV NEW YORK STATE RES FOUND.
 Query Match 14.7%; Score 227; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 RESULT 1313
 ID ADU66687 standard; peptide; 42 AA.
 DE Human FAM Gluc-(4) peptide.
 PN US2004235768-A1.
 PD 25-NOV-2004.
 PA (KORN/) KORNECKI E.
 PA (SOBO/) SOBOCKA M B.
 Query Match 14.7%; Score 227; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 RESULT 1314
 ID AAM31100 standard; peptide; 50 AA.
 DE Platelet membrane glycoprotein F11 fragment.
 PN US5665701-A.
 PD 09-SEP-1997.
 PA (UTNY) UNIV NEW YORK STATE RES FOUND.
 Query Match 14.7%; Score 227; DB 2; Length 50;
 Best Local Similarity 89.8%; Pred. No. 2.3e-09;
 RESULT 1315
 ID AAB61480 standard; protein; 325 AA.
 DE Human CTH protein.

PN WO200100672-A1.
 PD 04-JAN-2001.
 PA (MTIL-) MILLENNIUM PHARM INC.
 Query Match 14.6%; Score 225; DB 4; Length 325;
 Best Local Similarity 28.5%; Pred. No. 2.9e-08;
 RESULT 1316
 ID ADG39844 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #5.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA/) PENA C E A.
 PA (GUOX/) GUO X.
 PA (SHIM/) SHIMKETS R A.
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (SPYT/) SPYTEK K A.
 PA (MEHR/) MEHRABAN F.
 PA (TOPP/) TOPPER J N.
 PA (MALY/) MALYANKAR U M.
 PA (NASS/) WASSERMAN S M.
 PA (EDIN/) EDINGER S R.
 PA (SMIT/) SMITHSON G.
 PA (GUNT/) GUNTHER E.
 PA (KOMU/) KOMIVES L.
 Query Match 13.9%; Score 214.5; DB 7; Length 1708;
 Best Local Similarity 29.2%; Pred. No. 1.2e-06;
 RESULT 1317
 ID ADS10483 standard; protein; 2537 AA.
 DE Human therapeutic protein - SEQ ID 720.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 13.9%; Score 214.5; DB 8; Length 2537;
 Best Local Similarity 29.2%; Pred. No. 1.9e-06;
 RESULT 1318
 ID ADS98860 standard; protein; 2537 AA.
 DE Protein factor discovery related human contig polypeptide, SEQ ID 1124.
 PN WO2004087874-A2.
 PD 14-OCT-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 13.9%; Score 214.5; DB 8; Length 2537;
 Best Local Similarity 29.2%; Pred. No. 1.9e-06;
 RESULT 1319
 ID ABU12083 standard; protein; 2572 AA.
 DE Human NOV25b CG93858-02 protein SEQ ID 86.
 PN WO200281625-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 13.9%; Score 214.5; DB 6; Length 2572;
 Best Local Similarity 29.2%; Pred. No. 1.9e-06;
 RESULT 1320
 ID ADK60225 standard; protein; 2673 AA.
 DE Angiogenesis differentially expressed protein GS-P52.
 PN FR2836687-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 Query Match 13.9%; Score 214.5; DB 8; Length 2673;
 Best Local Similarity 29.2%; Pred. No. 2e-06;
 RESULT 1321
 ID ADK60526 standard; protein; 2673 AA.
 DE Angiogenesis differentially expressed protein GS-P52.
 PN FR2836686-A1.
 PD 05-SEP-2003.
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 Query Match 13.9%; Score 214.5; DB 8; Length 2673;
 Best Local Similarity 29.2%; Pred. No. 2e-06;
 RESULT 1322
 ID ADP73149 standard; protein; 2673 AA.
 DE Angiogenesis inhibitor human protein sequence, GS-P52.
 PN FR2843753-A1.

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PD 27-FEB-2004.
PA (GENE//) GENE S.
PA (ALMS//) AL M S.
Query Match
Best Local Similarity 13.9%; Score 214.5; DB 8; Length 2673;
Pred. No. 2e-06;
RESULT 1323
ID ABU69135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PD WO20029504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 13.9%; Score 214.5; DB 6; Length 4495;
Pred. No. 3.7e-06;
RESULT 1324
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOV43c SEQ ID NO:1002.
PD WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 13.9%; Score 214.5; DB 8; Length 4495;
Pred. No. 3.7e-06;
RESULT 1325
ID AD008273 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PD US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO//) ALSOBROOK J P.
PA (ANDE//) ANDERSON D W.
PA (BOLD//) BOLDOG F L.
PA (BURG//) BURGESS C E.
PA (CASM//) CASMAN S J.
PA (CHAP//) CHAPOVAL A.
PA (EDIN//) EDINGER S R.
PA (GERL//) GERLACH V.
PA (GORM//) GORMAN L.
PA (GUNT//) GUNTHER E.
PA (GUOX//) GUO X S.
PA (KEKU//) KEKUDA R.
PA (LEPL//) LEPLEY D M.
PA (LILU//) LI L.
PA (LIUX//) LIU X.
PA (MALY//) MALYANKAR U M.
PA (MILL//) MILLER C E.
PA (MILT//) MILLET I.
PA (PADI//) PADIGARU M.
PA (PATT//) PATTURAJAN M.
PA (PENNA//) PENNA C E A.
PA (RIEG//) RIEGER D K.
PA (SHEN//) SHENOT S G.
PA (SHIM//) SHIMKETS R A.
PA (SPYT//) SPYTER K A.
PA (TAUP//) TAUPIER R J.
PA (VERN//) VERNET C A M.
PA (VOSS//) VOSS E Z.
PA (ZERR//) ZERHUSEN B D.
Query Match
Best Local Similarity 13.9%; Score 214.5; DB 8; Length 4495;
Pred. No. 3.7e-06;
RESULT 1326
ID ADK40856 standard; peptide; 42 AA.
DE Human FAM, Glu-C proteolytic fragment.
PD US6699688-B1.
PD 02-MAR-2004.
PA (UNIV) UNIV NEW YORK STATE RRS FOUND.
Query Match
Best Local Similarity 13.9%; Score 214; DB 8; Length 42;
Pred. No. 1.7e-08;
RESULT 1327
ID ADU66696 standard; peptide; 42 AA.
DE Human FAM endoproteinase GluC proteolytic peptide.
PD US2004235768-A1.
PD 25-NOV-2004.
PA (KORN//) KORNECKI E.
PA (SOBO//) SOBOCKA M B.
Query Match
Best Local Similarity 13.9%; Score 214; DB 8; Length 42;
Pred. No. 1.7e-08;
RESULT 1328
ID ABG03933 standard; protein; 1240 AA.
DE Novel human diagnostic protein #3924.
PD WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 4; Length 1240;
Pred. No. 5.6e-07;
RESULT 1329
ID ABA47771 standard; protein; 1336 AA.
DE Human thrombospondin protein, BTL.012.
PD WO200174852-A2.
PD 11-OCT-2001.
PA (FAB) BAYER CORP.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 5; Length 1336;
Pred. No. 1.1e-06;
RESULT 1330
ID ADG39841 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #2.
PD US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA//) PENNA C E A.
PA (GUOX//) GUO X.
PA (SHIM//) SHIMKETS R A.
PA (PADI//) PADIGARU M.
PA (KEKU//) KEKUDA R.
PA (SPYT//) SPYTER K A.
PA (MEHR//) MEHRABAN F.
PA (TOPE//) TOPPER J N.
PA (MALY//) MALYANKAR U M.
PA (WASS//) WASSERMAN S M.
PA (EDIN//) EDINGER S R.
PA (SMIT//) SMITHSON G.
PA (GUNT//) GUNTHER E.
PA (KOMU//) KOMUVES L.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 7; Length 1708;
Pred. No. 1.4e-06;
RESULT 1331
ID ADG39840 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #1.
PD US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA//) PENNA C E A.
PA (GUOX//) GUO X.
PA (SHIM//) SHIMKETS R A.
PA (PADI//) PADIGARU M.
PA (KEKU//) KEKUDA R.
PA (SPYT//) SPYTER K A.
PA (MEHR//) MEHRABAN F.
PA (TOPE//) TOPPER J N.
PA (MALY//) MALYANKAR U M.
PA (WASS//) WASSERMAN S M.
PA (EDIN//) EDINGER S R.
PA (SMIT//) SMITHSON G.
PA (GUNT//) GUNTHER E.
PA (KOMU//) KOMUVES L.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 7; Length 1708;
Pred. No. 1.4e-06;
RESULT 1332
ID ABU12084 standard; protein; 1902 AA.
DE Human NOV25c CG56914-03 protein SEQ ID 88.
PD WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 6; Length 1902;
Pred. No. 1.6e-06;
RESULT 1333
ID ADH72108 standard; protein; 1902 AA.
DE Human protein of the invention NOV43d SEQ ID NO:1004.
PD WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
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Query Match
Best Local Similarity 13.8%; Score 213.5; DB 8; Length 1902;
RESULT 1334
ID ABE1658 standard; protein; 1953 AA.
DE G-coupled protein receptor related polypeptide, SEQ ID No 88.
PN W0200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 7; Length 1953;
RESULT 1335
ID ADJ9397 standard; protein; 1953 AA.
DE Human G-coupled protein receptor-related protein #44.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILU/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENNA/) PENNA C E A.
PA (SHEN/) SHENY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAI K.
PA (BURG/) BURGESS C E.
PA (MALT/) MALTANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 8; Length 1953;
RESULT 1336
ID ADJ83136 standard; protein; 3645 AA.
DE Human hemiscitin protein - SEQ ID 127.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATR/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILU/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILT/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 8; Length 1953;
RESULT 1337
ID AEB94406 standard; protein; 5622 AA.
DE Human hemiscitin/FIBL-6 protein, SEQ ID NO: 128.
PN US2005176662-A1.
PD 11-AUG-2005.
PA (UWMI-) UNIV MIMI.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 9; Length 5622;
RESULT 1338
ID ABB60991 standard; protein; 5635 AA.
DE Novel human protein. SEQ ID 78.
PN W0200250105-A1.
PD 27-JUN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (GLAX ) GLAXO GROUP LTD.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 5; Length 5635;
RESULT 1339
ID ADJ70089 standard; protein; 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target Segid1895.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 7; Length 5636;
RESULT 1340
ID ADJ83137 standard; protein; 5636 AA.
DE Human hemiscitin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATR/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILU/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILT/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 7; Length 5636;
RESULT 1341
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2835687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 13.8%; Score 213.5; DB 8; Length 5636;

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RESULT 1342
ID AD60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN PR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 13.8%; Score 213.5; DB 8; Length 5636;
Best Local Similarity 29.2%; Pred. No. 5.6e-06;
RESULT 1343
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 13.8%; Score 213.5; DB 8; Length 5636;
Best Local Similarity 29.2%; Pred. No. 5.6e-06;
RESULT 1344
ID AD74434 standard; protein; 4126 AA.
DE Human hemicentin protein lacking part of the N-terminus.
PN US6867291-B1.
PD 15-MAR-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 13.8%; Score 212.5; DB 9; Length 4126;
Best Local Similarity 29.2%; Pred. No. 4.6e-06;
RESULT 1345
ID AEB34668 standard; protein; 4126 AA.
DE Human hemicentin protein, SEQ ID 4.
PN US2005164277-A1.
PD 28-JUL-2005.
PA (TURN/) TURNER C A.
PA (MATH/) MATHUR B.
PA (DONO/) DONOHO G.
Query Match 13.8%; Score 212.5; DB 9; Length 4126;
Best Local Similarity 29.2%; Pred. No. 4.6e-06;
RESULT 1346
ID AD74432 standard; protein; 5518 AA.
DE Human hemicentin protein.
PN US6867291-B1.
PD 15-MAR-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 13.8%; Score 212.5; DB 9; Length 5518;
Best Local Similarity 29.2%; Pred. No. 6.5e-06;
RESULT 1347
ID AEB34666 standard; protein; 5518 AA.
DE Human hemicentin protein, SEQ ID 2.
PN US2005164277-A1.
PD 28-JUL-2005.
PA (TURN/) TURNER C A.
PA (MATH/) MATHUR B.
PA (DONO/) DONOHO G.
Query Match 13.8%; Score 212.5; DB 9; Length 5518;
Best Local Similarity 29.2%; Pred. No. 6.5e-06;
RESULT 1348
ID AAU18038 standard; protein; 294 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 183.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.6%; Score 210; DB 4; Length 294;
Best Local Similarity 26.3%; Pred. No. 3.2e-07;
RESULT 1349
ID ADB31662 standard; protein; 294 AA.
DE Human novel protein SEQ ID NO 183.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.6%; Score 210; DB 7; Length 294;
Best Local Similarity 26.3%; Pred. No. 3.2e-07;
RESULT 1350
ID AAB08940 standard; protein; 245 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:97.

PN WO20017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.5%; Score 208.5; DB 3; Length 245;
Best Local Similarity 30.4%; Pred. No. 3.4e-07;
RESULT 1351
ID AAB08926 standard; protein; 246 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:83.
PN WO20017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.5%; Score 208.5; DB 3; Length 246;
Best Local Similarity 30.4%; Pred. No. 3.4e-07;
RESULT 1352
ID AAY72878 standard; protein; 352 AA.
DE Human PRO5723 protein encoded by DNA82361 CDNA clone.
PN WO200116319-A2.
PD 08-MAR-2001.
PA (GETH-) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1353
ID AAB50930 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH-) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1354
ID AAB65294 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:505.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH-) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1355
ID ABB84956 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:280.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH-) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 5; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1356
ID ABB95562 standard; protein; 352 AA.
DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH-) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERR/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANU/) PANU J.
PA (PAON/) PAONTI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 13.4%; Score 207.5; DB 5; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1357
ID ADV31956 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN WO200193983-A1.
PD 13-DEC-2001.

[illegible]

RESULT 1367	ID	ABU59334	standard; protein; 352 AA.	
	DE	Human secreted/transmembrane protein, #177.		
	PN	US2002027162-A1.		
	PD	06-FEB-2003.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1368	ID	ABO26031	standard; protein; 352 AA.	
	DE	Human PRO5723 polypeptide.		
	PN	US2002127576-A1.		
	PD	12-SEP-2002.		
	PA	(GETH) GENENTECH INC.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1369	ID	ABU82155	standard; protein; 352 AA.	
	DE	Novel human secreted and transmembrane protein PRO5723.		
	PN	US2003088063-A1.		
	PD	08-MAY-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1370	ID	ABU59040	standard; protein; 352 AA.	
	DE	Human secreted/transmembrane protein, #177.		
	PN	US2002142961-A1.		
	PD	03-OCT-2002.		
	PA	(GETH) GENENTECH INC.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1371	ID	ABU92418	standard; protein; 352 AA.	
	DE	Novel human secreted and transmembrane protein PRO5723.		
	PN	US2003022187-A1.		
	PD	30-JAN-2003.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1372	ID	ABU59483	standard; protein; 352 AA.	
	DE	Novel human secreted or transmembrane protein PRO3301.		
	PN	US2003027985-A1.		
	PD	06-FEB-2003.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1373	ID	ABU92249	standard; protein; 352 AA.	
	DE	Novel human secreted and transmembrane protein PRO5723.		
	PN	US2003017476-A1.		
	PD	23-JAN-2003.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1374	ID	ABU10955	standard; protein; 352 AA.	
	DE	Human PRO polypeptide #141.		
	PN	US2002123463-A1.		
	PD	05-SEP-2002.		
	PA	(GETH) GENENTECH INC.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1375	ID	ABU61707	standard; protein; 352 AA.	
	DE	Novel human secreted and transmembrane protein PRO5723.		
	PN	US2002177164-A1.		
	PD	28-NOV-2002.		
	PA	(GETH) GENENTECH INC.		
	Query Match		13.4%; Score 207.5; DB 6; Length 352;	
	Best Local Similarity		26.7%; Pred. No. 6.1e-07;	
RESULT 1376	ID	ABU86646	standard; protein; 352 AA.	
	DE	Human secreted and transmembrane polypeptide PRO5723.		
	PN	US2002197615-A1.		
	PD	26-DEC-2002.		

PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1377
ID ABO34160 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1378
ID ABJ72335 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1379
ID ADA38016 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1380
ID ADA21702 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1381
ID ADA10489 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO5723.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1382
ID ADA18033 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1383
ID ADA28141 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1384
ID ADA94721 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1385
ID ADA38946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1386
ID ABJ72463 standard; protein; 352 AA.
PN US2003027988-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1387
ID ADA93067 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1388
ID ABO34358 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO 5723.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1389
ID ABO53246 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1390
ID ADA22628 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1391
ID ABO22616 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1392
ID ADA06794 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #141.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1393
ID ABJ72165 standard; protein; 352 AA.
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1394
ID ADA39487 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1395
ID ADB83706 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4% Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7% Pred. No. 6.1e-07;
RESULT 1396
ID ADB80812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200308068-A1.

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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1397
ID ADB73353 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1398
ID ADB96513 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1399
ID ADB78435 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1400
ID ADB85083 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1401
ID ADB78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1402
ID ADB87255 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1403
ID ADB84837 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1404
ID ADB83952 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1405
ID ADB73107 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1406
ID ADC57985 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1407
ID ADC53749 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1408
ID ADC12216 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1409
ID ADC56638 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1410
ID ADC11683 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1411
ID ADC36945 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1412
ID ADC21935 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1413
ID ADC49966 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1414
ID ADC49165 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1415
ID ADC49682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088071-A1.
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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1416
ID ADC47543 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1417
ID ADC14805 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1418
ID ADC47288 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1419
ID ADD08337 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1420
ID ADC82162 standard; protein: 352 AA.
DE Human PRO polypeptide #141.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1421
ID ADD07804 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1422
ID ADC78163 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1423
ID ADC82695 standard; protein: 352 AA.
DE Human PRO polypeptide #141.
PN US2003058633-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1424
ID ADD06398 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1425

ID ADD10569 standard; protein: 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1426
ID ADD08875 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1427
ID ADC77917 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1428
ID ADD07124 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1429
ID ADD11529 standard; protein: 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1430
ID ADC83371 standard; protein: 352 AA.
DE Human PRO polypeptide #141.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1431
ID ADD50880 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1432
ID ADD13380 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003059437-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1433
ID ADD51126 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1434
ID ADD55478 standard; protein: 352 AA.
DE Human PRO polypeptide #141.
PN US2003077593-A1.

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PD 24-APR-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1435
ID ADD37322 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1436
ID ADD56436 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US200307594-A1.
PD 24-APR-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1437
ID ADD50607 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1438
ID ADD54874 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1439
ID ADD50361 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1440
ID ADD51372 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1441
ID ADE31893 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1442
ID ADE27028 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1443
ID ADE26495 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1444
ID ADE67432 standard; protein; 352 AA.
DE Human PRO5723 amino acid sequence SEQ ID NO:505.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1445
ID ADE94085 standard; protein; 352 AA.
DE Immune disease treatment/diagnosis related PRO5723.
PN US2003082199-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1446
ID ADI35686 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1447
ID ADI00179 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1448
ID ADC48919 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1449
ID ADE21090 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1450
ID ADE05934 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1451
ID ADD75163 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1452
ID ADD75909 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1453
ID ADE85141 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100722-A1.
PD 29-MAY-2003.
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PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1454	
ID	ADE20598 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100738-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1455	
ID	ADE20844 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100734-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1456	
ID	ADE39141 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003096362-A1.
PD	22-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1457	
ID	ADE05688 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100727-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1458	
ID	ADD73671 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100711-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1459	
ID	ADP78513 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100737-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1460	
ID	ADB41530 standard; protein; 352 AA.
DE	Human secreted/transmembrane PRO polypeptide #140.
PN	US2003100497-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1461	
ID	ADE21336 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100736-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1462	
ID	ADD77451 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100732-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1463	
ID	ADE20598 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100733-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1464	
ID	ADD75663 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100064-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1465	
ID	ADD74179 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100708-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1466	
ID	ADD74425 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100709-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1467	
ID	ADD76155 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100718-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1468	
ID	ADD85647 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100721-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1469	
ID	ADB05196 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100726-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1470	
ID	ADD75409 standard; protein; 352 AA.
DE	Human PRO polypeptide #108.
PN	US2003100714-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1471	
ID	ADD76953 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100715-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;
RESULT 1472	
ID	ADD77451 standard; protein; 352 AA.
DE	Novel human secreted and transmembrane protein PRO5723.
PN	US2003100732-A1.
PD	29-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	13.4%; Score 207.5; DB 8;
Best Local Similarity	Pred. No. 6.1e-07;

Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1472
ID ADD86721 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1473
ID ADD78189 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1474
ID ADD77697 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1475
ID ADD77943 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1476
ID ADD85401 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1477
ID ADD73933 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1478
ID ADD74671 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1479
ID ADD77199 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1480
ID ADD85893 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1481
ID ADE05442 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1482
ID ADD74917 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1483
ID ADF35631 standard; protein: 352 AA.
DE Human PRO5723 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1484
ID ADG11881 standard; protein: 352 AA.
DE Human PRO5723 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1485
ID ADG05729 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1486
ID ADG27283 standard; protein: 352 AA.
DE Human PRO polypeptide #108.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1487
ID ADG11346 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1488
ID ADG12125 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1489
ID ADF94682 standard; protein: 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 8; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1490
ID ADG06778 standard; protein: 352 AA.

DE Human PRO polypeptide #108.
 PN US200309696-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1491
 ID ADH39122 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003096965-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1492
 ID ADH19751 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein PRO5723.
 PN US200328656-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1493
 ID ADH21244 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein PRO5723.
 PN US200324358-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1494
 ID ADH20284 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein PRO5723.
 PN US2003219856-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1495
 ID ADH43713 standard; protein; 352 AA.
 DE Human PRO polypeptide #140.
 PN US2003224984-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1496
 ID ADG34212 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2004006206-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1497
 ID ADI33682 standard; protein; 352 AA.
 DE Human PRO polypeptide #108.
 PN US2003096960-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1498
 ID ADH69776 standard; protein; 352 AA.
 DE Human PRO polypeptide #108.
 PN US2004019183-A1.
 PD 29-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1499
 ID ADI29937 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003096961-A1.

PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;
 RESULT 1500
 ID ADM27334 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2004044179-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.4%; Score 207.5; DB 8; Length 352;
 Best Local Similarity 26.7%; Pred. No. 6.1e-07;

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OM protein - protein search, using sw model

Run on: May 16, 2006, 07:01:24 ; Search time 47 Seconds

(without alignments)
525.958 Million cell updates/sec

Title: US-10-785-433-1

Perfect score: 1544
Sequence: 1 MGTAYQVERKLLCFITAIL.....YQPSANSEGEFKQTSSFLV 299

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1544	100.0	299	2	US-09-188-930-331
2	1544	100.0	299	2	US-09-462-270-2
3	1544	100.0	299	2	US-09-254-465A-1
4	1544	100.0	299	2	US-09-312-283C-189
5	1544	100.0	299	2	US-09-312-283C-331
6	1544	100.0	299	2	US-09-907-794A-119
7	1544	100.0	299	2	US-09-905-125A-119
8	1544	100.0	299	2	US-09-902-775A-119
9	1544	100.0	299	2	US-09-397-243D-3
10	1544	100.0	299	2	US-09-906-700-119
11	1544	100.0	299	2	US-09-903-603A-119
12	1544	100.0	299	2	US-09-904-920A-119
13	1544	100.0	299	2	US-09-909-064-119
14	1544	100.0	299	2	US-09-905-381A-119
15	1544	100.0	299	2	US-09-906-618-119
16	1544	100.0	299	2	US-09-953-499-1
17	1544	100.0	299	2	US-09-906-646-119
18	1544	100.0	299	2	US-09-904-462-119
19	1544	100.0	299	2	US-09-903-736A-119
20	1544	100.0	299	2	US-09-906-722A-119
21	1532	99.2	299	2	US-09-188-930-189
22	1372	88.9	263	2	US-09-254-465A-25
23	1372	88.9	263	2	US-09-953-499-25
24	1355	87.8	260	2	US-09-254-465A-23
25	1355	87.8	260	2	US-09-953-499-23
26	1073.5	69.5	300	2	US-09-254-465A-10
27	1073.5	69.5	300	2	US-09-397-243D-12

28	1073.5	69.5	300	2	US-09-953-499-10	Sequence 10, Appli
29	1042.5	67.5	205	2	US-09-462-270-4	Sequence 4, Appli
30	910	58.9	193	2	US-09-397-243D-4	Sequence 173, App
31	576	37.3	134	2	US-09-312-283C-173	Sequence 173, App
32	569	36.9	134	2	US-09-188-930-173	Sequence 76, Appl
33	429	27.8	298	2	US-09-152-060-76	Sequence 76, Appl
34	429	27.8	298	2	US-09-852-797-76	Sequence 76, Appl
35	429	27.8	298	2	US-09-853-161-76	Sequence 76, Appl
36	429	27.8	298	2	US-10-058-993-76	Sequence 76, Appl
37	424	27.5	310	2	US-09-907-794A-423	Sequence 423, App
38	424	27.5	310	2	US-09-905-125A-423	Sequence 423, App
39	424	27.5	310	2	US-09-902-775A-423	Sequence 423, App
40	424	27.5	310	2	US-09-906-700-423	Sequence 423, App
41	424	27.5	310	2	US-09-903-603A-423	Sequence 423, App
42	424	27.5	310	2	US-09-904-920A-423	Sequence 423, App
43	424	27.5	310	2	US-09-909-064-423	Sequence 423, App
44	424	27.5	310	2	US-09-905-381A-423	Sequence 423, App
45	424	27.5	310	2	US-09-906-618-423	Sequence 423, App
46	424	27.5	310	2	US-09-906-646-423	Sequence 423, App
47	424	27.5	310	2	US-09-904-462-423	Sequence 423, App
48	424	27.5	310	2	US-09-902-736A-423	Sequence 423, App
49	424	27.5	310	2	US-10-033-301-20	Sequence 420, Appl
50	424	27.5	310	2	US-09-906-722A-423	Sequence 423, App
51	412	26.7	76	2	US-09-397-243D-9	Sequence 9, Appli
52	409	26.5	76	2	US-09-397-243D-11	Sequence 11, Appli
53	404	26.2	312	2	US-09-254-465A-9	Sequence 9, Appli
54	404	26.2	312	2	US-09-907-794A-64	Sequence 64, Appl
55	404	26.2	312	2	US-09-905-125A-64	Sequence 64, Appl
56	404	26.2	312	2	US-09-902-775A-64	Sequence 64, Appl
57	404	26.2	312	2	US-09-906-700-64	Sequence 64, Appl
58	404	26.2	312	2	US-09-903-603A-64	Sequence 64, Appl
59	404	26.2	312	2	US-09-904-920A-64	Sequence 64, Appl
60	404	26.2	312	2	US-09-909-064-64	Sequence 64, Appl
61	404	26.2	312	2	US-09-905-381A-64	Sequence 64, Appl
62	404	26.2	312	2	US-09-906-618-64	Sequence 64, Appl
63	404	26.2	312	2	US-09-953-499-9	Sequence 9, Appli
64	404	26.2	312	2	US-09-906-646-64	Sequence 64, Appl
65	404	26.2	312	2	US-09-904-462-64	Sequence 64, Appl
66	404	26.2	312	2	US-09-902-736A-64	Sequence 64, Appl
67	404	26.2	312	2	US-09-906-722A-64	Sequence 64, Appl
68	281.5	18.2	318	2	US-09-068-051A-32	Sequence 32, Appl
69	279	18.1	316	2	US-09-397-243D-13	Sequence 13, Appl
70	272.5	17.6	319	1	US-08-597-495B-22	Sequence 22, Appl
71	272.5	17.6	319	2	US-09-068-051A-22	Sequence 22, Appl
72	272.5	17.6	319	2	US-09-336-536-67	Sequence 67, Appl
73	272.5	17.6	319	2	US-09-254-465A-6	Sequence 6, Appli
74	272.5	17.6	319	2	US-09-953-499-6	Sequence 26, Appl
75	272	17.6	273	2	US-09-254-465A-26	Sequence 26, Appl
76	272	17.6	273	2	US-09-953-499-26	Sequence 26, Appl
77	269	17.4	270	2	US-09-254-465A-24	Sequence 24, Appl
78	269	17.4	270	2	US-09-953-499-24	Sequence 24, Appl
79	227	14.7	42	2	US-09-397-243D-6	Sequence 6, Appli
80	227	14.7	50	1	US-08-342-449-11	Sequence 11, Appl
81	214	13.9	42	2	US-09-397-243D-15	Sequence 15, Appl
82	212.5	13.8	412	2	US-09-953-096-4	Sequence 4, Appli
83	212.5	13.8	5518	2	US-09-953-096-2	Sequence 2, Appli
84	207.5	13.4	352	2	US-09-991-181-505	Sequence 505, App
85	207.5	13.4	352	2	US-09-990-444-505	Sequence 505, App
86	207.5	13.4	352	2	US-09-997-333-505	Sequence 505, App
87	207.5	13.4	352	1	US-08-992-598-805	Sequence 505, App
88	207.5	13.4	365	1	US-08-979-424-3	Sequence 3, Appli
89	207.5	13.4	365	2	US-09-272-96-2	Sequence 2, Appli
90	207.5	13.4	365	2	US-09-949-016-6064	Sequence 6064, Ap
91	207.5	13.4	383	2	US-09-949-016-11050	Sequence 11050, A
92	203.5	13.2	365	2	US-08-928-183B-2	Sequence 2, Appli
93	202.5	13.1	315	2	US-09-324-541-2	Sequence 28, Appl
94	202	13.1	315	2	US-09-910-174B-28	Sequence 28, Appl
95	202	13.1	315	2	US-09-620-461-28	Sequence 28, Appl
96	201	13.0	387	2	US-09-175-928-2	Sequence 2, Appli
97	197	12.8	365	2	US-09-899-634C-4	Sequence 4, Appli
98	196	12.7	261	2	US-09-899-634C-2	Sequence 2, Appli
99	196	12.7	373	2	US-09-991-181-503	Sequence 503, App
100	196	12.7	373	2	US-09-999-833A-59	Sequence 59, Appl

101	196	12.7	373	2	US-09-990-444-503	Sequence 503, App	174	171	11.1	1059	2	US-09-906-722A-290	Sequence 290, App
102	196	12.7	373	2	US-09-997-333-503	Sequence 503, App	175	171	11.1	1091	2	US-08-986-485-5	Sequence 5, App11
103	196	12.7	373	2	US-09-992-598-503	Sequence 503, App	176	171	11.1	1119	2	US-09-907-794A-294	Sequence 294, App
104	196	12.7	373	2	US-10-020-445A-59	Sequence 59, App1	177	171	11.1	1119	2	US-09-905-125A-294	Sequence 294, App
105	194	12.6	365	2	US-08-928-383B-23	Sequence 23, App1	178	171	11.1	1119	2	US-09-902-775A-294	Sequence 294, App
106	194	12.6	365	2	US-08-928-383B-24	Sequence 24, App1	179	171	11.1	1119	2	US-09-906-700-294	Sequence 294, App
107	189	12.2	365	2	US-08-928-383B-26	Sequence 26, App1	180	171	11.1	1119	2	US-09-903-603A-294	Sequence 294, App
108	182	11.8	329	2	US-10-104-047-3709	Sequence 3709, App	181	171	11.1	1119	2	US-09-904-920A-294	Sequence 294, App
109	181	11.7	1101	2	US-08-986-485-2	Sequence 2, App11	182	171	11.1	1119	2	US-09-909-064-294	Sequence 294, App
110	180.5	11.7	316	2	US-09-999-833A-137	Sequence 137, App	183	171	11.1	1119	2	US-09-905-381A-294	Sequence 294, App
111	180.5	11.7	316	2	US-10-020-445A-137	Sequence 137, App	184	171	11.1	1119	2	US-09-906-618-294	Sequence 294, App
112	179	11.6	340	2	US-09-651-200-2	Sequence 2, App11	185	171	11.1	1119	2	US-09-906-646-294	Sequence 294, App
113	179	11.6	441	2	US-09-651-200-4	Sequence 4, App11	186	171	11.1	1119	2	US-09-904-462-294	Sequence 294, App
114	179	11.6	534	2	US-09-651-200-6	Sequence 6, App11	187	171	11.1	1119	2	US-09-906-722A-294	Sequence 294, App
115	179	11.6	534	2	US-09-651-200-4	Sequence 24, App1	188	171	11.1	1119	2	US-09-906-722A-294	Sequence 294, App
116	178.5	11.6	316	2	US-09-910-174B-24	Sequence 24, App1	189	169	10.9	338	2	US-09-778-510-4	Sequence 4, App11
117	178.5	11.6	316	2	US-09-620-461-24	Sequence 24, App1	190	168.5	10.9	466	2	US-09-604-107A-8	Sequence 8, App11
118	178.5	11.6	316	2	US-09-915-789A-1	Sequence 1, App11	191	168	10.9	317	2	US-10-104-047-3036	Sequence 3036, App
119	178.5	11.6	321	2	US-09-254-465A-2	Sequence 2, App11	192	167.5	10.8	615	1	US-08-752-307B-9	Sequence 9, App11
120	178.5	11.6	321	2	US-09-953-489-2	Sequence 2, App11	193	167.5	10.8	615	2	US-09-707-802-9	Sequence 9, App11
121	178.5	11.6	321	2	US-09-999-833A-52	Sequence 52, App1	194	167.5	10.8	615	2	US-09-991-326-9	Sequence 9, App11
122	178.5	11.6	501	1	US-10-020-445A-52	Sequence 52, App1	195	167.5	10.8	1297	2	US-09-540-245A-17	Sequence 17, App1
123	178.5	11.6	501	1	US-08-408-095-31	Sequence 31, App1	196	167.5	10.8	1297	2	US-10-289-776-17	Sequence 17, App1
124	178.5	11.6	847	2	US-09-949-002-328	Sequence 328, App	197	167.5	10.8	1571	2	US-08-956-991-11	Sequence 11, App1
125	177.5	11.5	862	2	US-09-949-002-427	Sequence 427, App	198	167.5	10.8	1910	2	US-08-956-991-2	Sequence 2, App11
126	176	11.4	390	1	US-08-979-424-1	Sequence 1, App11	199	166.5	10.8	334	2	US-09-336-536-39	Sequence 39, App1
127	176	11.4	390	2	US-09-907-794A-39	Sequence 39, App1	200	165	10.7	335	2	US-09-949-016-7591	Sequence 7591, App
128	176	11.4	390	2	US-09-905-125A-39	Sequence 39, App1	201	161	10.4	344	1	US-08-602-725-34	Sequence 34, App1
129	176	11.4	390	2	US-09-902-775A-39	Sequence 39, App1	202	161	10.4	335	2	US-09-936-536-40	Sequence 40, App1
130	176	11.4	390	2	US-09-906-700-39	Sequence 39, App1	203	160.5	10.4	2596	2	US-09-548-473B-6	Sequence 6, App11
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132	176	11.4	390	2	US-09-904-920A-39	Sequence 39, App1	205	158	10.2	607	2	US-09-707-802-12	Sequence 12, App1
133	176	11.4	390	2	US-09-909-064-39	Sequence 39, App1	206	158	10.2	837	2	US-09-991-326-15	Sequence 12, App1
134	176	11.4	390	2	US-09-905-381A-39	Sequence 39, App1	207	157.5	10.2	313	2	US-09-949-016-6515	Sequence 6515, App
135	176	11.4	390	2	US-09-906-618-39	Sequence 39, App1	208	157	10.2	333	2	US-09-700-997-4	Sequence 4, App11
136	176	11.4	390	2	US-09-906-646-39	Sequence 39, App1	209	157	10.2	334	2	US-09-700-997-3	Sequence 3, App11
137	176	11.4	390	2	US-09-904-462-39	Sequence 39, App1	210	157	10.2	344	2	US-09-999-833A-523	Sequence 523, App
138	176	11.4	390	2	US-09-902-736A-39	Sequence 39, App1	211	157	10.2	334	2	US-10-020-445A-523	Sequence 523, App
139	176	11.4	390	2	US-09-906-722A-39	Sequence 39, App1	212	156	10.1	884	2	US-09-949-016-10605	Sequence 10605, App
140	176	11.4	398	2	US-09-778-510-6	Sequence 6, App11	213	155.5	10.1	819	2	US-09-949-016-11044	Sequence 11044, App
141	174	11.3	398	2	US-09-907-794A-84	Sequence 84, App1	214	154.5	10.0	482	1	US-08-752-307B-7	Sequence 7, App11
142	174	11.3	398	2	US-09-905-125A-84	Sequence 84, App1	215	154.5	10.0	482	2	US-09-707-802-7	Sequence 7, App11
143	174	11.3	398	2	US-09-902-775A-84	Sequence 84, App1	216	154.5	10.0	462	2	US-09-991-326-7	Sequence 7, App11
144	174	11.3	398	2	US-09-906-700-84	Sequence 84, App1	217	154.5	10.0	465	1	US-08-752-307B-5	Sequence 5, App11
145	174	11.3	398	2	US-09-903-603A-84	Sequence 84, App1	218	154.5	10.0	465	2	US-09-707-802-5	Sequence 5, App11
146	174	11.3	398	2	US-09-904-920A-84	Sequence 84, App1	219	154.5	10.0	465	2	US-09-991-326-5	Sequence 5, App11
147	174	11.3	398	2	US-09-909-064-84	Sequence 84, App1	220	154	10.0	588	2	US-09-949-016-10547	Sequence 10547, App
148	174	11.3	398	2	US-09-905-381A-84	Sequence 84, App1	221	154	10.0	848	2	US-09-961-403-44	Sequence 44, App1
149	174	11.3	398	2	US-09-906-618-84	Sequence 84, App1	222	154	10.0	1070	2	US-09-961-403-3	Sequence 3, App11
150	174	11.3	398	2	US-09-906-646-84	Sequence 84, App1	223	153.5	9.9	888	1	US-08-261-304-2	Sequence 2, App11
151	174	11.3	398	2	US-09-904-462-84	Sequence 84, App1	224	153	9.9	780	1	US-08-232-538-14	Sequence 14, App1
152	174	11.3	398	2	US-09-902-736A-84	Sequence 84, App1	225	153	9.9	780	1	US-08-786-164-14	Sequence 14, App1
153	174	11.3	398	2	US-09-906-722A-84	Sequence 84, App1	226	153	9.9	1260	2	US-08-506-296B-21	Sequence 21, App1
154	174	11.3	432	2	US-09-778-510-2	Sequence 2, App11	227	153	9.9	1338	2	US-08-750-141A-3	Sequence 3, App11
155	173.5	11.2	316	2	US-09-915-789A-3	Sequence 3, App11	228	153	9.9	1338	2	US-09-119-014D-6	Sequence 6, App11
156	173.5	11.2	1395	2	US-09-540-245A-15	Sequence 15, App1	229	152	9.8	334	1	US-08-414-657D-44	Sequence 44, App1
157	173.5	11.2	1395	2	US-10-288-776-15	Sequence 15, App1	230	152	9.8	335	1	US-08-414-657D-2	Sequence 2, App11
158	173	11.2	1709	2	US-09-949-016-10503	Sequence 10503, App	231	152	9.8	335	1	US-08-414-657D-41	Sequence 41, App1
159	172.5	11.2	341	2	US-09-336-536-29	Sequence 29, App1	232	152	9.8	335	2	US-09-135-080-2	Sequence 2, App11
160	172.5	11.2	370	2	US-09-336-536-28	Sequence 28, App1	233	152	9.8	338	1	US-08-414-657D-60	Sequence 60, App11
161	172	11.1	650	2	US-10-104-047-3395	Sequence 3395, App	234	152	9.8	338	2	US-09-135-080-8	Sequence 8, App11
162	171	11.1	1059	2	US-09-907-794A-290	Sequence 290, App	235	152	9.8	338	2	US-09-976-594-404	Sequence 404, App
163	171	11.1	1059	2	US-09-905-125A-290	Sequence 290, App	236	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
164	171	11.1	1059	2	US-09-902-775A-290	Sequence 290, App	237	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
165	171	11.1	1059	2	US-09-906-700-290	Sequence 290, App	238	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
166	171	11.1	1059	2	US-09-903-603A-290	Sequence 290, App	239	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
167	171	11.1	1059	2	US-09-904-920A-290	Sequence 290, App	240	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
168	171	11.1	1059	2	US-09-909-064-290	Sequence 290, App	241	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
169	171	11.1	1059	2	US-09-905-381A-290	Sequence 290, App	242	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
170	171	11.1	1059	2	US-09-906-618-290	Sequence 290, App	243	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
171	171	11.1	1059	2	US-09-906-646-290	Sequence 290, App	244	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
172	171	11.1	1059	2	US-09-904-462-290	Sequence 290, App	245	152	9.8	891	2	US-09-976-594-404	Sequence 404, App
173	171	11.1	1059	2	US-09-902-736A-290	Sequence 290, App	246	152	9.8	1253	2	US-08-506-296B-14	Sequence 14, App1

247	150.5	9.7	349	2	US-09-924-103-4	Sequence 4, Appl1	330	143.5	9.3	444	2	US-09-404-578-5	Sequence 5, Appl1
248	150.5	9.7	1501	1	US-08-447-464-3	Sequence 3, Appl1	331	143.5	9.3	504	2	US-09-949-016-7020	Sequence 7020, Ap
249	150.5	9.7	1501	1	US-08-716-679-3	Sequence 3, Appl1	332	143.5	9.3	504	2	US-09-991-181-119	Sequence 119, Ap
250	150	9.7	642	1	US-08-217-299-1	Sequence 1, Appl1	333	143.5	9.3	504	2	US-09-990-444-119	Sequence 119, Ap
251	150	9.7	698	1	US-08-602-725-36	Sequence 36, Appl1	334	143.5	9.3	504	2	US-09-997-333-119	Sequence 119, Ap
252	150	9.7	702	1	US-09-949-016-6484	Sequence 6484, Ap	335	143.5	9.3	504	2	US-09-992-598-119	Sequence 119, Ap
253	150	9.7	734	1	US-08-389-459A-17	Sequence 17, Appl1	336	143.5	9.3	511	2	US-09-949-016-10054	Sequence 10054, A
254	150	9.7	734	2	US-08-987-867A-17	Sequence 17, Appl1	337	143	9.3	310	1	US-08-414-657D-45	Sequence 45, Appl1
255	150	9.7	740	2	US-09-949-016-8168	Sequence 8168, Ap	338	143	9.3	338	1	US-08-414-657D-42	Sequence 42, Appl1
256	149	9.7	450	2	US-09-907-794A-320	Sequence 320, App	339	143	9.3	338	2	US-08-414-657D-43	Sequence 43, Appl1
257	149	9.7	450	2	US-09-905-125A-320	Sequence 320, App	340	143	9.3	338	2	US-09-135-080-4	Sequence 5, Appl1
258	149	9.7	450	2	US-09-902-775A-320	Sequence 320, App	341	142	9.2	464	2	US-08-800-825A-5	Sequence 5, Appl1
259	149	9.7	450	2	US-09-906-700-320	Sequence 320, App	342	142	9.2	464	2	US-08-348-006B-5	Sequence 5, Appl1
260	149	9.7	450	2	US-09-903-603A-320	Sequence 320, App	343	143	9.3	1911	1	US-08-800-825A-5	Sequence 5, Appl1
261	149	9.7	450	2	US-09-904-920A-320	Sequence 320, App	344	143	9.3	1911	2	US-09-158-657-5	Sequence 5, Appl1
262	149	9.7	450	2	US-09-909-064-320	Sequence 320, App	345	143	9.3	1913	4	PCT-US94-10166-5	Sequence 5, Appl1
263	149	9.7	450	2	US-09-905-381A-320	Sequence 320, App	346	143	9.3	1953	4	US-09-917-254-92	Sequence 92, Appl1
264	149	9.7	450	2	US-09-906-618-320	Sequence 320, App	347	142.5	9.2	289	2	US-09-310-463-12	Sequence 12, Appl1
265	149	9.7	450	2	US-09-906-646-320	Sequence 320, App	348	142	9.2	289	2	US-08-842-248A-12	Sequence 12, Appl1
266	149	9.7	450	2	US-09-904-462-320	Sequence 320, App	349	142	9.2	321	6	US-09-835-17	Patent No. 5169835
267	149	9.7	450	2	US-09-902-736A-320	Sequence 320, App	350	142	9.2	388	1	US-08-429-742-4	Sequence 4, Appl1
268	149	9.7	450	2	US-09-906-722A-320	Sequence 320, App	351	142	9.2	464	1	US-08-602-725-32	Sequence 32, Appl1
269	149	9.7	450	2	PCT-US93-00031-19	Sequence 19, Appl1	352	142	9.2	464	2	US-09-949-016-5116	Sequence 6116, Ap
270	149	9.7	644	4	US-09-903-00031-21	Sequence 21, Appl1	353	141.5	9.2	464	2	US-09-949-016-7525	Sequence 7525, Ap
271	149	9.7	647	2	US-08-482-073-5	Sequence 5, Appl1	354	141.5	9.2	315	1	US-08-414-657D-47	Sequence 47, Appl1
272	149	9.7	647	2	US-08-482-073-5	Sequence 5, Appl1	355	141.5	9.2	337	1	US-08-442-043A-18	Sequence 18, Appl1
273	149	9.7	647	2	US-09-982-262C-92	Sequence 92, Appl1	356	141.5	9.2	337	2	US-09-560-639-6	Sequence 6, Appl1
274	149	9.7	647	4	PCT-US93-00031-11	Sequence 11, Appl1	357	141.5	9.2	337	2	US-08-441-893A-18	Sequence 18, Appl1
275	149	9.7	647	4	PCT-US93-00031-23	Sequence 23, Appl1	358	141.5	9.2	342	2	US-09-032-337-7	Sequence 37, Appl1
276	149	9.7	735	4	PCT-US93-00031-15	Sequence 15, Appl1	359	141.5	9.2	567	2	US-09-560-639-7	Sequence 39, Appl1
277	149	9.7	736	4	US-08-482-073-6	Sequence 6, Appl1	360	141.5	9.2	567	2	US-09-173-151A-24	Sequence 24, Appl1
278	149	9.7	739	2	PCT-US93-00031-9	Sequence 9, Appl1	361	141.5	9.2	567	2	US-09-032-337-19	Sequence 39, Appl1
279	149	9.7	739	2	PCT-US93-00031-9	Sequence 9, Appl1	362	141.5	9.2	626	2	US-09-949-016-6213	Sequence 6213, Ap
280	149	9.7	740	4	US-09-949-016-10595	Sequence 17, Appl1	363	141.5	9.2	664	2	US-09-949-016-7850	Sequence 7850, Ap
281	148.5	9.6	1248	2	US-09-949-016-10595	Sequence 10595, A	364	141	9.1	34	1	US-08-342-449-8	Sequence 8, Appl1
282	148.5	9.6	1248	2	US-08-340-011-5	Sequence 5, Appl1	365	141	9.1	868	1	US-08-374-834-1	Sequence 1, Appl1
283	148.5	9.6	1311	1	US-08-901-710-5	Sequence 5, Appl1	366	141	9.1	868	1	US-08-644-271-1	Sequence 1, Appl1
284	148.5	9.6	1311	1	US-08-901-710-5	Sequence 5, Appl1	367	141	9.1	868	2	US-09-077-955-1	Sequence 1, Appl1
285	148.5	9.6	1311	1	US-08-901-710-5	Sequence 5, Appl1	368	141	9.1	868	2	US-10-016-283-1	Sequence 1, Appl1
286	148	9.6	1021	2	US-09-169-079-5	Sequence 5, Appl1	369	141	9.1	1024	2	US-09-949-002-123	Sequence 523, App
287	148	9.6	1021	2	US-08-417-025-3	Sequence 3, Appl1	370	141	9.1	1461	2	US-09-976-594-531	Sequence 531, App
288	147.5	9.6	1021	2	US-09-949-002-363	Sequence 363, App	371	140.5	9.1	252	1	US-08-414-657D-57	Sequence 57, Appl1
289	147.5	9.6	1021	2	US-09-205-258-947	Sequence 947, App	372	140	9.1	890	1	US-08-445-640-2	Sequence 2, Appl1
290	147.5	9.6	227	2	US-10-004-860-947	Sequence 48, Appl1	373	140	9.1	890	2	US-08-170-558-2	Sequence 2, Appl1
291	147.5	9.6	246	2	US-09-336-536-31	Sequence 31, Appl1	374	140	9.1	890	2	US-08-447-314-2	Sequence 2, Appl1
292	147.5	9.6	249	2	US-09-336-536-42	Sequence 42, Appl1	375	140	9.1	890	2	US-08-445-461-2	Sequence 2, Appl1
293	147.5	9.6	662	4	PCT-US95-08493-13	Sequence 13, Appl1	376	139	9.0	869	2	US-09-223-490-2	Sequence 2, Appl1
294	146.5	9.5	308	1	US-08-414-657D-46	Sequence 46, Appl1	377	138.5	9.0	1745	2	US-09-949-016-11380	Sequence 89, Appl1
295	146.5	9.5	1651	2	US-09-540-245A-18	Sequence 18, Appl1	378	138	8.9	514	2	US-09-949-016-11380	Sequence 11380, A
296	146.5	9.5	1651	2	US-10-289-776-18	Sequence 10804, A	379	138	8.9	517	2	US-09-723-368-4	Sequence 4, Appl1
297	146.5	9.5	816	2	US-09-949-016-10904	Sequence 2, Appl1	380	138	8.9	605	1	US-08-752-307B-8	Sequence 8, Appl1
298	146	9.5	816	2	US-09-949-016-10904	Sequence 2, Appl1	381	138	8.9	605	1	US-09-707-802-8	Sequence 8, Appl1
299	146	9.5	4391	2	US-10-006-011A-2	Sequence 20, Appl1	382	138	8.9	605	2	US-09-991-336-8	Sequence 8, Appl1
300	145.5	9.4	215	2	US-08-414-657D-56	Sequence 56, Appl1	383	138	8.9	874	1	US-08-456-647B-6	Sequence 6, Appl1
301	145.5	9.4	252	1	US-08-414-657D-56	Sequence 56, Appl1	384	138	8.9	874	1	US-08-237-401A-6	Sequence 6, Appl1
302	145.5	9.4	1194	2	US-10-191-029-10	Sequence 10, Appl1	385	138	8.9	880	2	US-08-445-640-18	Sequence 18, Appl1
303	145	9.4	758	2	US-08-874-678-1	Sequence 1, Appl1	386	138	8.9	880	2	US-08-170-558-10	Sequence 10, Appl1
304	145	9.4	758	2	US-08-643-833-1	Sequence 1, Appl1	387	138	8.9	880	2	US-08-445-641-10	Sequence 10, Appl1
305	145	9.4	758	2	US-09-051-363-24	Sequence 24, Appl1	388	138	8.9	880	2	US-08-445-641-10	Sequence 10, Appl1
306	145	9.4	758	2	US-09-348-886-1	Sequence 1, Appl1	389	138	8.9	880	2	US-08-445-641-10	Sequence 10, Appl1
307	145	9.4	758	2	US-10-105-901A-1	Sequence 1, Appl1	390	138	8.9	880	2	US-08-445-641-10	Sequence 10, Appl1
308	145	9.4	802	2	US-09-173-151A-33	Sequence 33, Appl1	391	138	8.9	880	2	US-08-445-641-10	Sequence 10, Appl1
309	144.5	9.4	478	4	US-10-191-029-12	Sequence 12, Appl1	392	137.5	8.9	518	2	US-09-223-490-10	Sequence 20, Appl1
310	144	9.3	306	4	PCT-US95-08493-15	Sequence 15, Appl1	393	137	8.9	252	2	US-09-270-767-44627	Sequence 44627, A
311	144	9.3	860	4	PCT-US95-08493-19	Sequence 19, Appl1							
312	144	9.3	868	4	PCT-US95-08493-21	Sequence 21, Appl1							
313	144	9.3	1381	2	US-09-540-245A-16	Sequence 16, Appl1							
314	144	9.3	1381	2	US-10-289-776-16	Sequence 16, Appl1							
315	143.5	9.3	421	1	US-08-659-984A-1	Sequence 1, Appl1							
316	143.5	9.3	421	2	US-08-660-531-1	Sequence 1, Appl1							
317	143.5	9.3	421	2	US-09-404-578-1	Sequence 1, Appl1							
318	143.5	9.3	444	1	US-08-659-984A-5	Sequence 5, Appl1							
319	143.5	9.3	444	2	US-08-660-531-5	Sequence 5, Appl1							

393	136.5	8.8	191	2	US-09-270-767-33678	Sequence 33678, A	466	129.5	8.4	456	2	US-09-949-016-7564	Sequence 7564, Ap
394	136.5	8.8	191	2	US-09-270-767-48895	Sequence 48895, A	467	129.5	8.4	609	2	US-09-949-016-7747	Sequence 7747, Ap
395	136.5	8.8	434	2	US-09-540-245A-19	Sequence 19, Appl	468	129.5	8.4	609	2	US-09-949-016-7748	Sequence 7748, Ap
396	136.5	8.8	434	2	US-10-289-776-19	Sequence 19, Appl	469	129.5	8.4	609	2	US-09-949-016-7749	Sequence 7749, Ap
397	136.5	8.8	833	2	US-09-949-016-11496	Sequence 11496, A	470	129.5	8.4	609	2	US-09-949-016-7750	Sequence 7750, Ap
398	136.5	8.8	1180	2	US-09-949-016-6577	Sequence 6577, Ap	471	129.5	8.4	609	2	US-09-949-016-7751	Sequence 7751, Ap
399	136	8.8	526	1	US-08-471-570-4	Sequence 4, Appl	472	129.5	8.4	609	2	US-09-949-016-7752	Sequence 7752, Ap
400	136	8.8	652	1	US-08-471-570-10	Sequence 10, Appl	473	129.5	8.4	609	2	US-09-949-016-7753	Sequence 7753, Ap
401	135.5	8.8	292	2	US-09-800-729-175	Sequence 175, App	474	129.5	8.4	609	2	US-09-949-016-7754	Sequence 7754, Ap
402	135.5	8.8	805	2	US-08-985-526-34	Sequence 34, Appl	475	129.5	8.4	721	1	US-07-921-807B-5	Sequence 5, Appl1
403	135.5	8.8	806	2	US-08-443-861-5	Sequence 5, Appl1	476	129.5	8.4	721	1	US-08-441-944A-5	Sequence 5, Appl1
404	135.5	8.8	806	2	US-08-193-829B-5	Sequence 5, Appl1	477	129.5	8.4	721	2	US-08-439-992A-3	Sequence 3, Appl1
405	135.5	8.8	806	2	US-09-766-678-5	Sequence 5, Appl1	478	129.5	8.4	723	1	US-09-620-561-3	Sequence 3, Appl1
406	135.5	8.8	1367	1	US-07-813-593-4	Sequence 4, Appl1	479	129.5	8.4	723	1	US-07-620-029-4	Sequence 4, Appl1
407	135.5	8.8	1367	1	US-07-977-451-6	Sequence 6, Appl1	480	129.5	8.4	723	1	US-07-921-807B-6	Sequence 6, Appl1
408	135.5	8.8	1367	1	US-07-946-507-4	Sequence 4, Appl1	481	129.5	8.4	723	1	US-08-441-944A-6	Sequence 6, Appl1
409	135.5	8.8	1367	1	US-08-252-517-6	Sequence 6, Appl1	482	129.5	8.4	723	2	US-08-439-992A-4	Sequence 4, Appl1
410	135.5	8.8	1367	1	US-07-906-397A-6	Sequence 6, Appl1	483	129.5	8.4	723	2	US-09-620-561-4	Sequence 4, Appl1
411	135.5	8.8	1367	1	US-08-601-891-6	Sequence 6, Appl1	484	129.5	8.4	817	1	US-07-640-029-2	Sequence 2, Appl1
412	135.5	8.8	1367	1	US-08-443-861-2	Sequence 2, Appl1	485	129.5	8.4	817	1	US-07-921-807B-3	Sequence 3, Appl1
413	135.5	8.8	1367	1	US-09-021-324-6	Sequence 6, Appl1	486	129.5	8.4	820	1	US-08-441-944A-3	Sequence 3, Appl1
414	135.5	8.8	1367	2	US-08-193-829B-2	Sequence 2, Appl1	487	129.5	8.4	820	2	US-08-439-992A-1	Sequence 1, Appl1
415	135.5	8.8	1367	2	US-09-872-136B-6	Sequence 6, Appl1	488	129.5	8.4	820	2	US-09-620-561-1	Sequence 1, Appl1
416	135.5	8.8	1367	2	US-09-766-678-2	Sequence 2, Appl1	489	129.5	8.4	822	1	US-07-997-133-1	Sequence 1, Appl1
417	135.5	8.8	1367	2	US-09-919-408A-6	Sequence 6, Appl1	490	129.5	8.4	822	1	US-07-921-807B-4	Sequence 4, Appl1
418	135.5	8.8	1367	4	PCT-US92-02750-8	Sequence 8, Appl1	491	129.5	8.4	822	1	US-08-459-296-2	Sequence 2, Appl1
419	135.5	8.8	1367	4	PCT-US92-05401-6	Sequence 6, Appl1	492	129.5	8.4	822	1	US-08-441-944A-4	Sequence 4, Appl1
420	135.5	8.8	1367	4	PCT-US92-09893-6	Sequence 6, Appl1	493	129.5	8.4	822	1	US-08-451-822A-12	Sequence 12, Appl
421	134.5	8.7	306	1	US-08-147-772-4	Sequence 4, Appl1	494	129.5	8.4	822	2	US-08-439-992A-2	Sequence 2, Appl1
422	134.5	8.7	306	1	US-08-456-104-8	Sequence 8, Appl1	495	129.5	8.4	822	2	US-08-123-430-12	Sequence 12, Appl
423	134.5	8.7	306	1	US-08-101-624-25	Sequence 25, Appl	496	129.5	8.4	822	2	US-09-620-561-2	Sequence 2, Appl1
424	134.5	8.7	306	2	US-08-153-262-4	Sequence 4, Appl1	497	129	8.4	354	2	US-10-104-047-2965	Sequence 2965, Ap
425	134.5	8.7	306	2	US-08-479-744A-31	Sequence 31, Appl	498	129	8.4	368	1	US-08-445-640-6	Sequence 6, Appl1
426	134.5	8.7	306	2	US-08-280-757B-31	Sequence 31, Appl	499	129	8.4	368	2	US-08-170-558-6	Sequence 6, Appl1
427	134.5	8.7	306	2	US-09-159-135-4	Sequence 4, Appl1	500	129	8.4	368	2	US-08-447-314-6	Sequence 6, Appl1
428	134.5	8.7	306	2	US-09-450-798-4	Sequence 4, Appl1	501	129	8.4	368	2	US-08-445-461-6	Sequence 6, Appl1
429	134.5	8.7	306	2	US-09-425-762-31	Sequence 31, Appl	502	129	8.4	368	2	US-09-223-490-6	Sequence 6, Appl1
430	134.5	8.7	306	2	US-08-453-386A-4	Sequence 4, Appl1	503	128.5	8.3	322	2	US-09-667-135-2	Sequence 2, Appl1
431	134.5	8.7	306	2	US-09-206-132-8	Sequence 8, Appl1	504	128.5	8.3	322	2	US-09-610-174B-29	Sequence 29, Appl
432	134.5	8.7	306	2	US-09-425-516-31	Sequence 31, Appl	505	128.5	8.3	322	2	US-09-620-461-29	Sequence 29, Appl
433	134	8.7	640	2	US-09-949-016-7565	Sequence 7565, Ap	506	128.5	8.3	524	2	US-09-770-767-44009	Sequence 44009, A
434	133.5	8.6	398	2	US-09-189-035-6	Sequence 6, Appl1	507	128.5	8.3	488	2	US-08-166-7170-6	Sequence 6, Appl1
435	133.5	8.6	398	2	US-09-382-086-6	Sequence 6, Appl1	508	128	8.3	497	2	US-09-499-846-6	Sequence 6, Appl1
436	133.5	8.6	398	2	US-08-999-689A-5	Sequence 5, Appl1	509	128	8.3	497	2	US-09-499-846-6	Sequence 6, Appl1
437	133.5	8.6	419	6	5169835-2	Patent No. 5169835	510	128	8.3	497	2	US-09-499-846-6	Sequence 6, Appl1
438	133.5	8.6	661	1	US-08-232-538-12	Sequence 12, Appl	511	127.5	8.3	270	1	US-08-552-507-2	Sequence 2, Appl1
439	133.5	8.6	661	1	US-08-786-164-12	Sequence 6, Appl1	512	127.5	8.3	322	2	US-09-583-586-33	Sequence 33, Appl
440	133.5	8.6	687	1	US-08-232-538-6	Sequence 6, Appl1	513	127.5	8.3	322	2	US-09-823-038A-33	Sequence 33, Appl
441	133.5	8.6	687	1	US-08-786-164-6	Sequence 6, Appl1	514	127.5	8.3	347	2	US-09-667-135-4	Sequence 4, Appl1
442	133.5	8.6	687	2	US-09-427-353-2	Sequence 2, Appl1	515	127.5	8.3	424	6	5169835-6	Patent No. 5169835
443	132	8.5	352	2	US-09-999-833A-612	Sequence 612, App	516	127.5	8.3	449	2	US-09-310-463-38	Sequence 38, Appl
444	132	8.5	352	2	US-10-020-445A-612	Sequence 612, App	517	127.5	8.3	561	2	US-09-866-510-24	Sequence 24, Appl
445	132	8.5	1018	1	US-08-408-093-6	Sequence 6, Appl1	518	127.5	8.3	1106	2	US-09-866-510-14	Sequence 14, Appl
446	132	8.5	1018	1	US-08-408-420A-6	Sequence 6, Appl1	519	127.5	8.3	1106	2	US-08-180-195-2	Sequence 2, Appl1
447	132	8.5	1018	1	US-08-714-901-6	Sequence 6, Appl1	520	127.5	8.3	1106	1	US-08-168-917-2	Sequence 2, Appl1
448	132	8.5	1018	2	US-08-040-741-6	Sequence 6, Appl1	521	127.5	8.3	1106	1	US-08-477-329-2	Sequence 2, Appl1
449	132	8.5	1044	2	US-09-949-016-10321	Sequence 10321, A	522	127.5	8.3	1106	1	US-08-475-458-2	Sequence 2, Appl1
450	131.5	8.5	81	2	US-09-423-439-44	Sequence 44, Appl	523	127.5	8.3	1106	1	US-08-460-510-2	Sequence 2, Appl1
451	131.5	8.5	281	2	US-07-640-029-1	Sequence 1, Appl1	524	127.5	8.3	1106	1	US-08-460-510-2	Sequence 2, Appl1
452	131.5	8.5	1266	1	US-08-506-296B-4	Sequence 4, Appl1	525	127.5	8.3	1106	2	US-08-980-400-2	Sequence 2, Appl1
453	130.5	8.5	729	1	US-07-640-029-3	Sequence 3, Appl1	526	127.5	8.3	1106	2	US-08-980-400-2	Sequence 2, Appl1
454	130	8.4	529	2	US-09-383-586-31	Sequence 31, Appl	527	127.5	8.3	1106	2	US-08-462-728-4	Sequence 4, Appl1
455	130	8.4	529	2	US-09-823-038A-31	Sequence 31, Appl	528	127.5	8.3	1106	2	US-09-583-459A-2	Sequence 2, Appl1
456	129.5	8.4	212	2	US-09-949-016-10458	Sequence 10458, A	529	127.5	8.3	1106	2	US-09-583-459A-2	Sequence 2, Appl1
457	129.5	8.4	306	2	US-08-205-697A-17	Sequence 17, Appl	530	127.5	8.3	1106	2	US-09-883-449A-2	Sequence 2, Appl1
458	129.5	8.4	306	2	US-08-702-525-17	Sequence 17, Appl	531	127.5	8.3	1106	2	US-09-431-917-4	Sequence 4, Appl1
459	129.5	8.4	306	2	US-09-651-200-17	Sequence 17, Appl	532	127.5	8.3	1106	2	US-08-464-436-4	Sequence 4, Appl1
460	129.5	8.4	306	2	US-09-667-125-35	Sequence 35, Appl	533	127.5	8.3	1106	2	US-08-464-436-4	Sequence 4, Appl1
461	129.5	8.4	306	2	US-09-837-867A-17	Sequence 17, Appl	534	127.5	8.3	1106	2	US-09-866-510-16	Sequence 16, Appl
462	129.5	8.4	306	4	PCT-US95-02576-17	Sequence 17, Appl	535	127.5	8.3	1106	2	US-09-866-510-18	Sequence 18, Appl
463	129.5	8.4	417	2	US-09-949-016-6729	Sequence 32, Appl	536	127.5	8.3	1106	2	US-09-866-510-20	Sequence 20, Appl
464	129.5	8.4	439	2	US-09-383-586-32	Sequence 32, Appl	537	127.5	8.3	1106	2	US-09-866-510-22	Sequence 22, Appl
465	129.5	8.4	439	2	US-09-823-038A-32	Sequence 32, Appl	538	127.5	8.3	1106	4	PCT-US92-00730-2	Sequence 2, Appl1

539	127.5	8.3	1106	4	PCT-US92-00862-2	Sequence 2, Appl1	612	124.5	8.1	917	1	US-08-245-295-2	Sequence 2, Appl1
540	127	8.2	393	1	US-08-428-742-2	Sequence 2, Appl1	613	124.5	8.1	917	1	US-08-481-130-2	Sequence 2, Appl1
541	127	8.2	416	2	US-09-638-649-1	Sequence 1, Appl1	614	124.5	8.1	917	1	US-08-656-984A-2	Sequence 2, Appl1
542	127	8.2	416	2	US-08-755-235-2	Sequence 2, Appl1	615	124.5	8.1	917	1	US-08-485-604-2	Sequence 2, Appl1
543	127	8.2	416	2	US-09-638-648-1	Sequence 1, Appl1	616	124.5	8.1	917	1	US-08-487-595-2	Sequence 2, Appl1
544	127	8.2	668	1	US-08-233-538-13	Sequence 13, Appl1	617	124	8.0	26	2	US-09-397-243D-14	Sequence 14, Appl1
545	127	8.2	668	1	US-08-786-164-13	Sequence 13, Appl1	618	124	8.0	34	1	US-08-342-449-1	Sequence 1, Appl1
546	127	8.2	686	2	US-09-173-151A-4	Sequence 4, Appl1	619	124	8.0	302	2	US-09-789-697A-21	Sequence 21, Appl1
547	127	8.2	788	1	US-08-232-538-15	Sequence 15, Appl1	620	124	8.0	388	1	US-08-445-640-12	Sequence 12, Appl1
548	127	8.2	788	1	US-08-786-164-15	Sequence 15, Appl1	621	124	8.0	388	2	US-08-170-558-12	Sequence 12, Appl1
549	126.5	8.2	398	2	US-09-579-845-4	Sequence 4, Appl1	622	124	8.0	388	2	US-08-447-314-12	Sequence 12, Appl1
550	126.5	8.2	1447	2	US-09-041-886-25	Sequence 25, Appl1	623	124	8.0	388	2	US-08-445-461-12	Sequence 12, Appl1
551	126.5	8.2	1447	4	PCT-US94-05277-2	Sequence 2, Appl1	624	124	8.0	388	2	US-09-223-490-12	Sequence 12, Appl1
552	126	8.2	666	2	US-09-423-439-51	Sequence 51, Appl1	625	124	8.0	643	1	US-08-471-570-6	Sequence 6, Appl1
553	126	8.2	764	2	US-09-142-956B-14	Sequence 14, Appl1	626	124	8.0	769	1	US-08-471-570-6	Sequence 8, Appl1
554	126	8.2	767	1	US-08-874-678-2	Sequence 2, Appl1	627	123.5	8.0	262	2	US-10-104-047-1119	Sequence 3119, Ap
555	126	8.2	767	2	US-08-643-839-2	Sequence 2, Appl1	628	123.5	8.0	503	2	US-08-999-689A-6	Sequence 6, Appl1
556	126	8.2	767	2	US-09-348-886-2	Sequence 2, Appl1	629	123.5	8.0	503	2	US-09-944-807-4	Sequence 4, Appl1
557	126	8.2	767	2	US-10-105-901A-2	Sequence 2, Appl1	630	123.5	8.0	885	2	US-10-104-047-2946	Sequence 2946, Ap
558	126	8.2	1356	1	US-08-810-116-8	Sequence 8, Appl1	631	123.5	8.0	915	2	US-10-282-162-52	Sequence 52, Appl1
559	126	8.2	1356	1	US-07-930-548A-8	Sequence 8, Appl1	632	123.5	8.0	917	2	US-10-282-162-54	Sequence 54, Appl1
560	126	8.2	1356	2	US-09-098-707A-2	Sequence 2, Appl1	633	123.5	8.0	917	2	US-10-282-162-56	Sequence 56, Appl1
561	126	8.2	1356	2	US-09-483-539-2	Sequence 2, Appl1	634	123.5	7.9	299	2	US-09-651-200-15	Sequence 15, Appl1
562	126	8.2	1356	2	US-09-949-016-6198	Sequence 6198, Ap	635	122.5	7.9	646	2	US-09-949-016-6728	Sequence 6728, Ap
563	126	8.2	1356	2	US-10-100-405A-2	Sequence 2, Appl1	636	122.5	7.9	646	2	US-09-653-961-2	Sequence 2, Appl1
564	126	8.2	1356	2	US-10-022-939-2	Sequence 2, Appl1	637	122.5	7.9	646	2	US-09-653-961-4	Sequence 4, Appl1
565	126	8.2	1456	2	US-09-949-016-9853	Sequence 9853, Ap	638	122.5	7.9	826	2	US-09-877-730-16	Sequence 16, Appl1
566	125.5	8.1	398	1	US-08-091-519-2	Sequence 2, Appl1	639	122.5	7.9	904	2	US-09-877-730-6	Sequence 6, Appl1
567	125.5	8.1	398	1	US-08-442-043A-2	Sequence 2, Appl1	640	122.5	7.9	907	2	US-09-877-730-60	Sequence 2, Appl1
568	125.5	8.1	398	2	US-09-173-151A-26	Sequence 26, Appl1	641	122.5	7.9	915	2	US-10-282-162-66	Sequence 46, Appl1
569	125.5	8.1	398	2	US-09-461-908-2	Sequence 2, Appl1	642	122.5	7.9	917	2	US-10-282-162-68	Sequence 48, Appl1
570	125.5	8.1	398	2	US-08-441-893A-2	Sequence 2, Appl1	643	122.5	7.9	985	2	US-09-182-152-50	Sequence 50, Appl1
571	125.5	8.1	398	2	US-08-406-824A-8	Sequence 8, Appl1	644	122.5	7.9	985	2	US-09-877-730-64	Sequence 10, Appl1
572	125.5	8.1	398	2	US-09-921-667-8	Sequence 8, Appl1	645	122.5	7.9	991	2	US-09-877-730-12	Sequence 12, Appl1
573	125.5	8.1	398	4	PCT-US91-03478-2	Sequence 2, Appl1	646	122.5	7.9	1069	2	US-09-877-730-18	Sequence 2, Appl1
574	125.5	8.1	418	2	US-09-949-016-9458	Sequence 9458, Ap	647	122.5	7.9	1072	2	US-09-877-730-18	Sequence 18, Appl1
575	125.5	8.1	471	2	US-09-949-016-9042	Sequence 9042, Ap	648	122.5	7.9	1150	2	US-09-877-730-8	Sequence 8, Appl1
576	125.5	8.1	471	2	US-09-949-016-9043	Sequence 9043, Ap	649	122.5	7.9	1209	2	US-09-877-730-8	Sequence 2, Appl1
577	125.5	8.1	471	2	US-09-949-016-9043	Sequence 9043, Ap	650	122	7.9	216	2	US-09-291-289A-9	Sequence 2, Appl1
578	125.5	8.1	471	2	US-09-949-016-9044	Sequence 9044, Ap	651	122	7.9	256	2	US-09-949-016-7326	Sequence 7326, Ap
579	125.5	8.1	471	2	US-09-949-016-9045	Sequence 9045, Ap	652	122	7.9	351	4	PCT-US93-05703-2	Sequence 2, Appl1
580	125.5	8.1	471	2	US-09-949-016-9046	Sequence 9046, Ap	653	122	7.9	373	2	US-09-823-038A-60	Sequence 60, Appl1
581	125.5	8.1	471	2	US-09-949-016-9047	Sequence 9047, Ap	654	122	7.9	525	2	US-09-499-846-4	Sequence 4, Appl1
582	125.5	8.1	471	2	US-09-949-016-9048	Sequence 9048, Ap	655	122	7.9	525	2	US-09-499-846-8	Sequence 8, Appl1
583	125.5	8.1	471	2	US-09-949-016-9049	Sequence 9049, Ap	656	122	7.9	622	2	US-09-499-846-2	Sequence 2, Appl1
584	125.5	8.1	471	2	US-09-949-016-9050	Sequence 9050, Ap	657	122	7.9	668	2	US-09-173-151A-35	Sequence 35, Appl1
585	125.5	8.1	596	1	US-08-752-307B-13	Sequence 13, Appl1	658	122	7.9	771	2	US-09-818-247-4	Sequence 4, Appl1
586	125.5	8.1	596	2	US-09-707-802-13	Sequence 13, Appl1	659	121.5	7.9	404	2	US-09-949-016-31025	Sequence 11025, A
587	125.5	8.1	596	2	US-09-991-326-13	Sequence 13, Appl1	660	121.5	7.9	404	2	US-09-799-152-1	Sequence 1, Appl1
588	125.5	8.1	611	1	US-08-752-307B-10	Sequence 10, Appl1	661	121	7.8	490	2	US-09-667-135-28	Sequence 28, Appl1
589	125.5	8.1	611	2	US-09-707-802-10	Sequence 10, Appl1	662	121	7.8	771	2	US-08-434-000A-8	Sequence 8, Appl1
590	125.5	8.1	611	2	US-09-991-326-10	Sequence 10, Appl1	663	121	7.8	771	2	US-09-312-157-8	Sequence 8, Appl1
591	125.5	8.1	612	1	US-08-752-307B-11	Sequence 11, Appl1	664	121	7.8	771	2	US-09-717-888-8	Sequence 8, Appl1
592	125.5	8.1	612	2	US-09-707-802-11	Sequence 11, Appl1	665	120.5	7.8	240	2	US-09-049-672A-11	Sequence 11, Appl1
593	125.5	8.1	612	2	US-09-991-326-11	Sequence 11, Appl1	666	120.5	7.8	303	2	US-09-509-347-7	Sequence 7, Appl1
594	125.5	8.1	821	1	US-08-451-832A-13	Sequence 13, Appl1	667	120.5	7.8	404	2	US-09-638-649-3	Sequence 3, Appl1
595	125.5	8.1	821	2	US-08-323-430-13	Sequence 13, Appl1	668	120.5	7.8	404	2	US-09-638-648-3	Sequence 3, Appl1
596	125.5	8.1	1268	1	US-08-506-296B-28	Sequence 28, Appl1	669	119.5	7.7	302	2	US-09-877-730-14	Sequence 14, Appl1
597	125	8.1	553	1	US-08-661-052-15	Sequence 15, Appl1	670	119.5	7.7	332	2	US-09-949-016-4483	Sequence 8483, Ap
598	125	8.1	553	2	US-09-188-082-16	Sequence 16, Appl1	671	119.5	7.7	380	2	US-09-877-730-4	Sequence 4, Appl1
599	125	8.1	553	2	US-09-364-088-16	Sequence 16, Appl1	672	119.5	7.7	467	2	US-09-046-736-2	Sequence 2, Appl1
600	125	8.1	553	2	US-09-102-716-16	Sequence 16, Appl1	673	119.5	7.7	560	2	US-09-949-016-8293	Sequence 8293, Ap
601	124.5	8.1	140	2	US-08-986-485-4	Sequence 4, Appl1	674	119	7.7	651	2	US-09-270-767-44877	Sequence 21, Appl1
602	124.5	8.1	235	2	US-09-646-561-12	Sequence 12, Appl1	675	118.5	7.7	238	2	US-09-798-689-21	Sequence 8, Appl1
603	124.5	8.1	304	2	US-09-646-561-2	Sequence 2, Appl1	676	118.5	7.7	239	2	US-08-279-772A-8	Sequence 8, Appl1
604	124.5	8.1	320	2	US-08-205-697A-2	Sequence 2, Appl1	677	118.5	7.7	239	2	US-08-902-486-11	Sequence 11, Appl1
605	124.5	8.1	320	2	US-08-702-525-2	Sequence 2, Appl1	678	118.5	7.7	512	2	US-08-999-689A-7	Sequence 7, Appl1
606	124.5	8.1	320	2	US-09-837-867A-2	Sequence 2, Appl1	679	118.5	7.7	985	2	US-09-999-833A-211	Sequence 211, App
607	124.5	8.1	320	4	PCT-US95-02576-2	Sequence 2, Appl1	680	118.5	7.7	985	2	US-10-020-445A-211	Sequence 211, App
608	124.5	8.1	769	2	US-08-434-000A-10	Sequence 10, Appl1	681	118	7.6	489	2	US-09-667-135-10	Sequence 30, Appl1
609	124.5	8.1	769	2	US-09-312-157-10	Sequence 10, Appl1	682	118	7.6	795	2	US-09-949-016-7119	Sequence 7119, Ap
610	124.5	8.1	769	2	US-09-717-888-10	Sequence 10, Appl1	683	118	7.6	924	1	US-08-481-130-28	Sequence 28, Appl1
611	124.5	8.1	769	2	US-09-818-247-3	Sequence 3, Appl1	684	118	7.6	924	1	US-08-656-984A-28	Sequence 28, Appl1

685	118	7.6	924	1	US-08-485-604-28	Sequence 28, Appl	758	114.5	7.4	439	2	US-08-385-950-12	Sequence 12, Appl
686	118	7.6	924	1	US-08-487-595-38	Sequence 28, Appl	759	114.5	7.4	439	2	US-09-310-463-8	Sequence 8, Appl
687	117.5	7.6	328	2	US-09-560-639-9	Sequence 9, Appl	760	114.5	7.4	439	2	US-08-842-248A-8	Sequence 8, Appl
688	117.5	7.6	328	2	US-09-173-151A-25	Sequence 25, Appl	761	114.5	7.4	439	2	US-09-546-049-12	Sequence 12, Appl
689	117.5	7.6	328	2	US-09-032-337-45	Sequence 45, Appl	762	114.5	7.4	579	2	US-09-173-151A-2	Sequence 2, Appl
690	117.5	7.6	328	2	US-09-949-016-6424	Sequence 6424, Ap	763	114	7.4	405	2	US-08-755-235-4	Sequence 4, Appl
691	117.5	7.6	374	2	US-09-046-736-4	Sequence 4, Appl	764	114	7.4	630	1	US-08-752-307B-14	Sequence 14, Appl
692	117.5	7.6	403	2	US-09-638-649-5	Sequence 5, Appl	765	114	7.4	630	2	US-09-707-802-14	Sequence 14, Appl
693	117.5	7.6	403	2	US-09-638-648-5	Sequence 5, Appl	766	114	7.4	630	2	US-09-991-326-14	Sequence 14, Appl
694	117.5	7.6	440	2	US-08-759-628-4	Sequence 4, Appl	767	113.5	7.4	316	2	US-10-027-736A-17	Sequence 17, Appl
695	117.5	7.6	544	2	US-09-999-833A-259	Sequence 259, App	768	113.5	7.4	332	2	US-09-062-365-1	Sequence 1, Appl
696	117.5	7.6	544	2	US-10-020-445A-259	Sequence 259, App	769	113	7.3	447	2	US-09-746-311B-379	Sequence 379, App
697	117.5	7.6	556	2	US-09-560-639-8	Sequence 8, Appl	770	113	7.3	448	2	US-09-310-463-18	Sequence 18, Appl
698	117.5	7.6	589	2	US-09-866-510-12	Sequence 12, Appl	771	113	7.3	448	2	US-08-842-248A-18	Sequence 18, Appl
699	117.5	7.6	608	2	US-09-095-185-4	Sequence 4, Appl	772	113	7.3	448	2	US-09-949-016-6764	Sequence 6764, Ap
700	117.5	7.6	762	2	US-09-949-016-7568	Sequence 7568, Ap	773	113	7.3	455	2	US-09-949-016-7116	Sequence 7116, Ap
701	117.5	7.6	764	2	US-09-949-016-6254	Sequence 6254, Ap	774	113	7.3	489	2	US-09-310-463-14	Sequence 14, Appl
702	117.5	7.6	764	2	US-09-818-247-1	Sequence 1, Appl	775	113	7.3	489	2	US-08-842-248A-14	Sequence 14, Appl
703	117.5	7.6	816	2	US-09-949-016-8119	Sequence 8119, Ap	776	113	7.3	489	2	US-09-949-016-6765	Sequence 6765, Ap
704	117.5	7.6	1088	2	US-09-961-403-4	Sequence 4, Appl	777	113	7.3	652	2	US-09-310-463-4	Sequence 4, Appl
705	117.5	7.6	1089	1	US-08-180-195-36	Sequence 36, Appl	778	113	7.3	652	2	US-08-842-248A-4	Sequence 4, Appl
706	117.5	7.6	1089	1	US-08-168-917-36	Sequence 4, Appl	779	113	7.3	677	2	US-09-949-002-416	Sequence 416, App
707	117.5	7.6	1089	1	US-08-477-329-36	Sequence 36, Appl	780	113	7.3	729	1	US-08-070-165F-6	Sequence 6, Appl
708	117.5	7.6	1089	1	US-08-475-458-36	Sequence 36, Appl	781	113	7.3	729	1	US-08-885-418-6	Sequence 8, Appl
709	117.5	7.6	1089	1	US-08-460-510-4	Sequence 4, Appl	782	113	7.3	1140	2	US-09-579-692B-8	Sequence 11, Appl
710	117.5	7.6	1089	1	US-08-460-490-4	Sequence 4, Appl	783	112.5	7.3	259	2	US-09-560-639-11	Sequence 11, Appl
711	117.5	7.6	1089	2	US-08-980-400-36	Sequence 36, Appl	784	112.5	7.3	463	2	US-10-012-231A-160	Sequence 160, App
712	117.5	7.6	1089	2	US-08-462-728-2	Sequence 2, Appl	785	112.5	7.3	463	2	US-10-015-389A-160	Sequence 160, App
713	117.5	7.6	1089	2	US-09-583-459A-36	Sequence 36, Appl	786	112.5	7.3	463	2	US-10-006-768A-160	Sequence 160, App
714	117.5	7.6	1089	2	US-09-583-210-36	Sequence 36, Appl	787	112.5	7.3	463	2	US-10-015-671A-160	Sequence 160, App
715	117.5	7.6	1089	2	US-09-583-449A-36	Sequence 36, Appl	788	112.5	7.3	463	2	US-10-015-393A-160	Sequence 160, App
716	117.5	7.6	1089	2	US-09-435-059-36	Sequence 36, Appl	789	112.5	7.3	463	2	US-10-011-833A-160	Sequence 160, App
717	117.5	7.6	1089	2	US-08-461-917-2	Sequence 2, Appl	790	112.5	7.3	463	2	US-10-006-041A-160	Sequence 160, App
718	117.5	7.6	1089	2	US-08-464-436-2	Sequence 2, Appl	791	112.5	7.3	463	2	US-10-012-064A-160	Sequence 160, App
719	117.5	7.6	1089	2	US-08-464-436-2	Sequence 2, Appl	792	112.5	7.3	619	2	US-10-104-047-2048	Sequence 2048, Ap
720	117.5	7.6	1089	2	US-09-769-987-2	Sequence 2, Appl	793	112.5	7.3	806	2	US-09-383-630-3	Sequence 3, Appl
721	117.5	7.6	1089	2	US-09-866-510-2	Sequence 2, Appl	794	111.5	7.2	194	2	US-09-375-419-14	Sequence 14, Appl
722	117.5	7.6	1089	2	US-09-866-510-4	Sequence 4, Appl	795	111.5	7.2	217	2	US-09-291-299A-7	Sequence 7, Appl
723	117.5	7.6	1089	2	US-09-866-510-6	Sequence 6, Appl	796	111.5	7.2	623	2	US-09-949-016-1106	Sequence 1106, A
724	117.5	7.6	1089	2	US-09-866-510-8	Sequence 8, Appl	797	111.5	7.2	637	2	US-09-569-611C-35	Sequence 35, Appl
725	117.5	7.6	1089	2	US-09-866-510-10	Sequence 10, Appl	798	111.5	7.2	668	2	US-09-949-016-8139	Sequence 8139, Ap
726	117.5	7.6	1089	2	US-09-919-497-90	Sequence 90, Appl	799	111	7.2	22	2	US-09-397-2430-5	Sequence 5, Appl
727	117.5	7.6	1089	2	US-09-949-016-6703	Sequence 6703, Ap	800	111	7.2	194	2	US-08-630-172-14	Sequence 14, Appl
728	117.5	7.6	1089	4	PCT-US93-00730-4	Sequence 4, Appl	801	111	7.2	194	2	US-09-375-419-14	Sequence 14, Appl
729	117.5	7.6	1089	4	PCT-US93-00862-4	Sequence 4, Appl	802	111	7.2	269	2	US-10-000-489-78	Sequence 78, Appl
730	117	7.6	278	2	US-09-270-767-42034	Sequence 42034, A	803	111	7.2	330	1	US-08-525-864A-4	Sequence 4, Appl
731	117	7.6	599	1	US-08-463-163-3	Sequence 3, Appl	804	111	7.2	523	1	US-09-810-174B-11	Sequence 11, Appl
732	116.5	7.5	263	2	US-09-949-016-8484	Sequence 8484, Ap	805	111	7.2	523	1	US-09-620-461-11	Sequence 11, Appl
733	116.5	7.5	801	2	US-09-383-630-6	Sequence 6, Appl	806	111	7.2	581	1	US-08-724-394A-3	Sequence 3, Appl
734	116.5	7.5	803	2	US-09-412-554A-2	Sequence 2, Appl	807	111	7.2	721	1	US-08-070-165F-10	Sequence 10, Appl
735	116	7.5	216	2	US-09-291-399A-8	Sequence 8, Appl	808	111	7.2	731	1	US-08-885-418-18	Sequence 18, Appl
736	116	7.5	216	2	US-09-291-399A-10	Sequence 10, Appl	809	111	7.2	754	1	US-08-525-864A-2	Sequence 2, Appl
737	116	7.5	230	6	5169635-13	Patent No. 5169635	810	110.5	7.2	499	2	US-09-949-672A-11	Sequence 1, Appl
738	116	7.5	732	2	US-09-818-247-5	Sequence 5, Appl	811	110.5	7.2	738	2	US-08-478-208-32	Sequence 32, Appl
739	115.5	7.5	257	2	US-09-489-039A-13452	Sequence 13452, A	812	110.5	7.2	738	2	US-09-636-536-73	Sequence 73, Appl
740	115.5	7.5	280	2	US-09-270-767-43068	Sequence 43068, A	813	110	7.1	309	2	US-09-667-135-6	Sequence 6, Appl
741	115.5	7.5	292	2	US-09-561-200-16	Sequence 16, Appl	814	110	7.1	309	2	US-09-910-174B-7	Sequence 7, Appl
742	115.5	7.5	292	2	US-09-303-040-2	Sequence 2, Appl	815	110	7.1	309	2	US-09-620-461-7	Sequence 7, Appl
743	115.5	7.5	336	2	US-09-949-016-7714	Sequence 7714, Ap	816	110	7.1	431	2	US-09-038-832-2	Sequence 2, Appl
744	115.5	7.5	336	2	US-09-949-016-7715	Sequence 7715, Ap	817	110	7.1	431	2	US-09-038-832-4	Sequence 4, Appl
745	115.5	7.5	229	2	US-08-751-359-22	Sequence 22, Appl	818	110	7.1	447	2	US-09-949-016-8211	Sequence 8211, Ap
746	115	7.4	229	2	US-08-907-146B-32	Sequence 22, Appl	819	110	7.1	558	2	US-09-667-135-31	Sequence 31, Appl
747	115	7.4	229	2	US-09-910-174B-6	Sequence 8, Appl	820	109.5	7.1	258	2	US-09-926-738A-4	Sequence 14, Appl
748	115	7.4	290	2	US-09-620-461-8	Sequence 8, Appl	821	109.5	7.1	272	1	US-08-282-951-6	Sequence 17, Appl
749	115	7.4	290	2	US-09-451-291-1	Sequence 1, Appl	822	109.5	7.1	280	2	US-09-260-527-1	Sequence 1, Appl
750	115	7.4	290	2	US-09-645-069-4	Sequence 4, Appl	823	109.5	7.1	307	2	US-09-197-970B-3	Sequence 3, Appl
751	115	7.4	290	2	US-09-915-789A-17	Sequence 17, Appl	824	109.5	7.1	310	6	5434340-7	Patent No. 5434340
752	115	7.4	290	2	US-09-644-934-4	Sequence 4, Appl	825	109.5	7.1	470	2	US-09-238-741-4	Sequence 4, Appl
753	115	7.4	339	1	US-09-789-152-2	Sequence 2, Appl	826	109.5	7.1	477	1	US-08-359-705B-4	Sequence 4, Appl
754	115	7.4	340	1	US-08-633-148-2	Sequence 2, Appl	827	109.5	7.1	477	1	US-08-286-846A-4	Sequence 4, Appl
755	115	7.4	391	2	US-08-999-689A-8	Sequence 8, Appl	828	109.5	7.1	477	1	US-08-457-880A-4	Sequence 4, Appl
756	114.5	7.4	269	2	US-08-646-265A-109	Sequence 109, App	829	109.5	7.1	477	1	US-08-444-622A-4	Sequence 4, Appl
757	114.5	7.4	232	2	US-09-303-040-4	Sequence 4, Appl	830	109.5	7.1	477	2	US-08-942-562-4	Sequence 4, Appl

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832	109.5	7.1	483	2	US-09-949-016-8574	Sequence 8574, Ap	905	108	7.0	612	2	US-08-942-562-8	Sequence 8, Appli
833	109.5	7.1	500	2	US-10-104-047-2825	Sequence 2825, Ap	906	108	7.0	612	2	US-08-156-923-8	Sequence 8, Appli
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841	109.5	7.1	847	1	US-08-286-305A-5	Sequence 5, Appli	914	108	7.0	773	2	US-08-434-000A-2	Sequence 2, Appli
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843	109.5	7.1	847	1	US-08-440-816A-5	Sequence 5, Appli	916	108	7.0	773	2	US-09-717-888-2	Sequence 2, Appli
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846	109	7.1	248	2	US-09-109-207C-23	Sequence 23, Appli	919	108	7.0	839	1	US-08-286-846A-6	Sequence 6, Appli
847	109	7.1	248	2	US-09-296-005-23	Sequence 23, Appli	920	108	7.0	839	2	US-08-457-880A-6	Sequence 6, Appli
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852	109	7.1	276	2	US-09-949-016-7261	Sequence 7261, Ap	925	108	7.0	850	1	US-08-441-104A-7	Sequence 7, Appli
853	109	7.1	302	2	US-09-915-789A-18	Sequence 18, Appli	926	108	7.0	850	1	US-08-440-816A-7	Sequence 7, Appli
854	109	7.1	318	1	US-08-633-148-4	Sequence 4, Appli	927	108	7.0	850	2	US-09-417-381A-7	Sequence 7, Appli
855	109	7.1	526	2	US-09-269-939A-18	Sequence 18, Appli	928	108	7.0	1363	2	US-09-375-248-19	Sequence 19, Appli
856	109	7.1	640	2	US-09-907-794A-292	Sequence 292, App	929	107.5	7.0	247	2	US-09-910-174B-31	Sequence 31, Appli
857	109	7.1	640	2	US-09-905-125A-292	Sequence 292, App	930	107.5	7.0	256	2	US-09-526-738A-2	Sequence 2, Appli
858	109	7.1	640	2	US-09-902-775A-292	Sequence 292, App	931	107.5	7.0	479	2	US-09-723-368-2	Sequence 2, Appli
859	109	7.1	640	2	US-09-906-700-292	Sequence 292, App	932	107.5	7.0	479	2	US-09-949-016-6278	Sequence 6278, Ap
860	109	7.1	640	2	US-09-903-603A-292	Sequence 292, App	933	107.5	7.0	522	2	US-09-949-016-7563	Sequence 7563, Ap
861	109	7.1	640	2	US-09-904-920A-292	Sequence 292, App	934	107.5	7.0	653	2	US-09-991-181-229	Sequence 229, App
862	109	7.1	640	2	US-09-909-064-292	Sequence 292, App	935	107.5	7.0	653	2	US-09-990-444-229	Sequence 229, App
863	109	7.1	640	2	US-09-905-381A-292	Sequence 292, App	936	107.5	7.0	653	2	US-09-997-333-229	Sequence 229, App
864	109	7.1	640	2	US-09-906-618-292	Sequence 292, App	937	107.5	7.0	653	2	US-09-992-598-229	Sequence 229, App
865	109	7.1	640	2	US-09-906-646-292	Sequence 292, App	938	107.5	6.9	248	2	US-09-649-063-23	Sequence 23, Appli
866	109	7.1	640	2	US-09-904-462-292	Sequence 292, App	939	107	6.9	277	1	US-08-256-790-2	Sequence 2, Appli
867	109	7.1	640	2	US-09-902-736A-292	Sequence 292, App	940	107	6.9	278	1	US-08-432-016-5	Sequence 5, Appli
868	109	7.1	640	2	US-09-991-181-501	Sequence 501, App	941	107	6.9	278	1	US-08-684-594-5	Sequence 5, Appli
869	109	7.1	640	2	US-09-990-444-501	Sequence 501, App	942	107	6.9	318	6	5242798-5	Patent No. 5242798
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871	109	7.1	640	2	US-09-997-333-501	Sequence 501, App	944	106.5	6.9	394	2	US-09-656-952-10	Sequence 20, Appli
872	109	7.1	640	2	US-09-992-598-501	Sequence 501, App	945	106.5	6.9	477	1	US-08-432-016-3	Sequence 3, Appli
873	109	7.1	650	2	US-09-310-463-2	Sequence 2, Appli	946	106.5	6.9	477	1	US-08-684-594-3	Sequence 3, Appli
874	109	7.1	650	2	US-08-842-248A-2	Sequence 2, Appli	947	106.5	6.9	1617	2	US-09-784-358-16	Sequence 16, Appli
875	109	7.1	650	2	US-09-949-002-390	Sequence 390, App	948	106.5	6.9	1691	2	US-09-784-358-2	Sequence 2, Appli
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877	109	7.1	651	2	US-09-546-049-22	Sequence 22, Appli	950	106	6.9	251	1	US-08-398-612A-30	Sequence 30, Appli
878	108.5	7.0	240	1	US-08-471-570-12	Sequence 12, Appli	951	106	6.9	251	1	US-08-398-611A-30	Sequence 30, Appli
879	108.5	7.0	242	1	US-08-553-497A-26	Sequence 26, Appli	952	106	6.9	251	1	US-08-021-334A-30	Sequence 30, Appli
880	108.5	7.0	287	2	US-09-310-463-32	Sequence 32, Appli	953	106	6.9	251	2	US-09-027-449-27	Sequence 27, Appli
881	108.5	7.0	310	2	US-10-027-736A-15	Sequence 15, Appli	954	106	6.9	251	2	US-08-804-444A-27	Sequence 27, Appli
882	108.5	7.0	355	1	US-08-471-570-14	Sequence 14, Appli	955	106	6.9	251	2	US-09-026-985-27	Sequence 27, Appli
883	108.5	7.0	358	2	US-09-719-243-3	Sequence 3, Appli	956	106	6.9	251	2	US-09-121-952A-27	Sequence 27, Appli
884	108.5	7.0	394	2	US-09-855-323-17	Sequence 17, Appli	957	106	6.9	251	2	US-09-224-340A-27	Sequence 27, Appli
885	108.5	7.0	394	2	US-09-991-181-422	Sequence 422, App	958	106	6.9	251	2	US-09-355-014-27	Sequence 27, Appli
886	108.5	7.0	394	2	US-09-990-444-422	Sequence 422, App	959	106	6.9	252	2	US-08-398-613A-30	Sequence 30, Appli
887	108.5	7.0	394	2	US-09-997-333-422	Sequence 422, App	960	106	6.9	278	2	US-09-260-527-3	Sequence 3, Appli
888	108.5	7.0	394	2	US-09-992-598-422	Sequence 422, App	961	106	6.9	286	2	US-09-270-767-44618	Sequence 44618, A
889	108.5	7.0	466	2	US-09-698-705-11	Sequence 11, Appli	962	106	6.9	298	2	US-09-864-675-4	Sequence 4, Appli
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891	108.5	7.0	982	1	US-08-673-789-4	Sequence 4, Appli	964	106	6.9	421	2	US-09-569-611C-36	Sequence 36, Appli
892	108	7.0	248	1	US-08-887-352B-22	Sequence 22, Appli	965	106	6.9	466	2	US-09-944-807-12	Sequence 12, Appli
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897	108	7.0	248	2	US-10-113-996-22	Sequence 22, Appli	970	106	6.9	525	2	US-09-269-939A-6	Sequence 6, Appli
898	108	7.0	281	2	US-10-027-736A-67	Sequence 67, Appli	971	106	6.9	561	2	US-09-227-717-4	Sequence 23, Appli
899	108	7.0	310	2	US-09-976-594-807	Sequence 807, App	972	106	6.9	561	2	US-09-173-151A-23	Sequence 23, Appli
900	108	7.0	491	2	US-10-011-125A-2	Sequence 2, Appli	973	106	6.9	561	2	US-09-775-046-15	Sequence 15, Appli
901	108	7.0	612	1	US-08-359-705B-8	Sequence 8, Appli	974	106	6.9	698	2	US-09-579-692B-60	Sequence 60, Appli
902	108	7.0	612	1	US-08-286-846A-8	Sequence 8, Appli	975	106	6.9	1298	1	US-08-222-616-33	Sequence 33, Appli
903	108	7.0	612	1	US-08-457-880A-8	Sequence 8, Appli	976	106	6.9	1298	1	US-08-340-011-2	Sequence 2, Appli

977	105	6.9	1298	2	US-08-901-710-2	Sequence 2, Appli	1050	104.5	6.8	309	2	US-09-837-867A-21	Sequence 21, Appli
978	105	6.9	1298	2	US-08-446-648-33	Sequence 33, Appl	1051	104.5	6.8	309	2	US-09-206-132-4	Sequence 4, Appli
979	106	6.9	1298	2	US-09-982-610-33	Sequence 3, Appl	1052	104.5	6.8	309	2	US-09-441-111-13	Sequence 13, Appl
980	106	6.9	1298	2	US-09-169-079-2	Sequence 2, Appli	1053	104.5	6.8	309	2	US-09-441-111-18	Sequence 18, Appl
981	106	6.9	1298	4	PCT-US95-04228-33	Sequence 33, Appl	1054	104.5	6.8	309	2	US-09-441-111-24	Sequence 24, Appl
982	106	6.9	1362	1	US-08-874-678-33	Sequence 3, Appl	1055	104.5	6.8	309	2	US-09-425-516-23	Sequence 23, Appl
983	106	6.9	1362	2	US-08-643-839-33	Sequence 33, Appl	1056	104.5	6.8	309	4	PCT-US95-02576-21	Sequence 21, Appl
984	106	6.9	1362	2	US-09-348-886-33	Sequence 33, Appl	1057	104.5	6.8	314	2	US-08-205-697A-13	Sequence 13, Appl
985	106	6.9	1362	2	US-10-105-901A-33	Sequence 33, Appl	1058	104.5	6.8	314	2	US-08-702-525-13	Sequence 13, Appl
986	106	6.9	1363	1	US-08-340-011-4	Sequence 4, Appli	1059	104.5	6.8	314	2	US-09-837-867A-13	Sequence 13, Appl
987	106	6.9	1363	1	US-08-874-678-32	Sequence 32, Appl	1060	104.5	6.8	314	2	US-09-441-111-14	Sequence 14, Appl
988	106	6.9	1363	2	US-08-643-839-32	Sequence 32, Appl	1061	104.5	6.8	314	4	PCT-US95-02576-13	Sequence 13, Appl
989	106	6.9	1363	2	US-08-901-710-4	Sequence 4, Appli	1062	104.5	6.8	314	4	US-09-188-930-184	Sequence 184, App
990	106	6.9	1363	2	US-09-348-886-32	Sequence 32, Appl	1063	104.5	6.8	340	2	US-09-312-283C-184	Sequence 18, App
991	106	6.9	1363	2	US-09-375-248-2	Sequence 2, Appli	1064	104.5	6.8	356	2	US-09-441-111-11	Sequence 11, Appl
992	106	6.9	1363	2	US-09-169-079-4	Sequence 4, Appli	1065	104.5	6.8	356	2	US-09-441-111-11	Sequence 12, Appl
993	106	6.9	1363	2	US-10-105-901A-32	Sequence 32, Appl	1066	104.5	6.8	356	2	US-09-441-111-16	Sequence 16, Appl
994	106	6.9	1363	1	US-08-874-678-34	Sequence 34, Appl	1067	104.5	6.8	356	2	US-09-441-111-17	Sequence 17, Appl
995	106	6.9	1368	2	US-08-643-839-34	Sequence 34, Appl	1068	104.5	6.8	356	2	US-09-472-087-100	Sequence 100, App
996	106	6.9	1368	2	US-09-348-886-34	Sequence 34, Appl	1069	104.5	6.8	431	2	US-09-773-877B-27	Sequence 27, Appl
997	106	6.9	1368	2	US-10-105-901A-34	Sequence 34, Appl	1070	104.5	6.8	446	2	US-08-397-411-7	Sequence 7, Appli
998	105.5	6.8	274	2	US-09-570-367C-19	Sequence 19, Appl	1071	104.5	6.8	551	2	US-08-896-537A-2	Sequence 2, Appli
999	105.5	6.8	274	2	US-09-915-524-19	Sequence 19, Appl	1072	104.5	6.8	530	2	US-09-520-781-12	Sequence 12, Appl
1000	105.5	6.8	274	2	US-09-934-634-19	Sequence 19, Appl	1073	104.5	6.8	530	2	US-09-957-187-12	Sequence 12, Appl
1001	105.5	6.8	274	2	US-09-917-278-19	Sequence 19, Appl	1074	104.5	6.8	530	2	US-09-991-053-12	Sequence 12, Appl
1002	105.5	6.8	294	2	US-10-027-736A-18	Sequence 18, Appl	1075	104.5	6.8	530	2	US-07-958-140-2	Sequence 2, Appli
1003	105.5	6.8	329	2	US-09-651-200-19	Sequence 19, Appl	1076	104	6.7	243	1	US-07-958-140-2	Sequence 2, Appli
1004	105.5	6.8	329	2	US-09-646-561-7	Sequence 7, Appli	1077	104	6.7	243	4	PCT-US93-09166-2	Sequence 22, Appl
1005	105.5	6.8	357	2	US-09-949-016-9074	Sequence 9074, Ap	1078	104	6.7	244	1	US-08-553-937A-22	Sequence 22, Appl
1006	105.5	6.8	357	2	US-09-949-016-11040	Sequence 11040, A	1079	104	6.7	253	1	US-08-398-613A-58	Sequence 58, Appl
1007	105.5	6.8	365	2	US-09-949-016-5075	Sequence 9075, Ap	1080	104	6.7	253	1	US-08-398-611A-58	Sequence 58, Appl
1008	105.5	6.8	371	2	US-09-949-016-9073	Sequence 9073, Ap	1081	104	6.7	253	1	US-08-398-611A-58	Sequence 58, Appl
1009	105.5	6.8	442	1	US-08-460-036-2	Sequence 2, Appli	1082	104	6.7	253	1	US-08-491-334A-58	Sequence 44, Appl
1010	105.5	6.8	442	1	US-08-461-968A-2	Sequence 2, Appli	1083	104	6.7	253	2	US-09-027-449-44	Sequence 44, Appl
1011	105.5	6.8	442	1	US-08-461-968A-5	Sequence 5, Appli	1084	104	6.7	253	2	US-09-027-449-55	Sequence 44, Appl
1012	105.5	6.8	442	1	US-08-462-571-2	Sequence 2, Appli	1085	104	6.7	253	2	US-08-804-444A-44	Sequence 44, Appl
1013	105.5	6.8	442	1	US-08-462-571-5	Sequence 5, Appli	1086	104	6.7	253	2	US-08-804-444A-55	Sequence 44, Appl
1014	105.5	6.8	442	2	US-08-472-888A-2	Sequence 2, Appli	1087	104	6.7	253	2	US-09-026-985-44	Sequence 44, Appl
1015	105.5	6.8	442	2	US-08-472-888A-7	Sequence 7, Appli	1088	104	6.7	253	2	US-09-026-985-55	Sequence 44, Appl
1016	105.5	6.8	442	4	PCT-US96-10043-9	Sequence 9, Appli	1089	104	6.7	253	2	US-09-121-952A-44	Sequence 44, Appl
1017	105.5	6.8	442	4	PCT-US96-10043-12	Sequence 12, Appl	1090	104	6.7	253	2	US-09-121-952A-55	Sequence 44, Appl
1018	105.5	6.8	458	2	US-09-773-877B-22	Sequence 22, Appl	1091	104	6.7	253	2	US-09-234-340A-44	Sequence 44, Appl
1019	105.5	6.8	459	1	US-08-157-101A-7	Sequence 7, Appli	1092	104	6.7	253	2	US-09-234-340A-55	Sequence 44, Appl
1020	105.5	6.8	469	2	US-08-753-007A-8	Sequence 8, Appli	1093	104	6.7	253	2	US-09-355-014-44	Sequence 44, Appl
1021	105.5	6.8	469	2	US-09-398-456-8	Sequence 8, Appli	1094	104	6.7	253	2	US-09-355-014-55	Sequence 44, Appl
1022	105.5	6.8	526	2	US-09-910-174B-9	Sequence 9, Appli	1095	104	6.7	473	2	US-09-049-672A-4	Sequence 4, Appli
1023	105.5	6.8	526	2	US-09-620-461-9	Sequence 9, Appli	1096	104	6.7	1215	2	US-09-949-002-321	Sequence 321, App
1024	105.5	6.8	526	2	US-09-949-016-6122	Sequence 6122, Ap	1097	104	6.7	1367	2	US-09-487-558B-108	Sequence 108, App
1025	105.5	6.8	540	2	US-09-949-016-11644	Sequence 11644, A	1098	103.5	6.7	210	2	US-09-451-291-10	Sequence 2, Appl
1026	105.5	6.8	647	2	US-08-753-007A-32	Sequence 32, Appl	1099	103.5	6.7	220	1	US-09-915-789A-23	Sequence 23, Appl
1027	105.5	6.8	647	2	US-09-398-456-32	Sequence 32, Appl	1100	103.5	6.7	242	1	US-08-553-497A-28	Sequence 28, Appl
1028	105.5	6.8	757	2	US-09-818-247-2	Sequence 2, Appli	1101	103.5	6.7	245	2	US-09-645-069-2	Sequence 2, Appli
1029	105	6.8	308	6	5169835-15	Sequence 8, Appli	1102	103.5	6.7	245	2	US-09-644-934-2	Sequence 2, Appli
1030	105	6.8	315	2	US-08-332-562A-83	Sequence 83, Appl	1103	103.5	6.7	291	2	US-10-027-736A-19	Sequence 19, Appl
1031	105	6.8	315	2	US-09-949-016-7014	Sequence 7014, Ap	1104	103.5	6.7	315	2	US-09-949-016-11121	Sequence 11121, A
1032	105	6.8	317	2	US-10-027-736A-16	Sequence 16, Appl	1105	103.5	6.7	315	2	US-09-949-016-11182	Sequence 11182, A
1033	105	6.8	354	6	5169835-4	Sequence 16, Appl	1106	103.5	6.7	407	2	US-08-753-007A-6	Sequence 6, Appli
1034	104.5	6.8	144	6	5169835-8	Sequence 8, Appli	1107	103.5	6.7	407	2	US-09-398-456-6	Sequence 6, Appli
1035	104.5	6.8	191	2	US-09-270-767-32640	Sequence 68, Appl	1108	103.5	6.7	431	2	US-08-985-950-14	Sequence 14, Appl
1036	104.5	6.8	252	2	US-10-027-736A-68	Sequence 68, Appl	1109	103.5	6.7	431	2	US-08-985-950-20	Sequence 20, Appl
1037	104.5	6.8	273	2	US-08-397-411-6	Sequence 6, Appli	1110	103.5	6.7	431	2	US-09-546-049-14	Sequence 14, Appl
1038	104.5	6.8	299	2	US-09-310-463-30	Sequence 30, Appl	1111	103.5	6.7	431	2	US-09-546-049-20	Sequence 20, Appl
1039	104.5	6.8	303	2	US-09-651-200-23	Sequence 23, Appl	1112	103.5	6.7	527	2	US-09-910-174B-10	Sequence 10, Appl
1040	104.5	6.8	303	2	US-09-441-411-15	Sequence 15, Appl	1113	103.5	6.7	527	2	US-09-620-461-10	Sequence 10, Appl
1041	104.5	6.8	303	2	US-08-456-104-4	Sequence 4, Appli	1114	103.5	6.7	597	2	US-09-746-311B-381	Sequence 381, App
1042	104.5	6.8	309	1	US-08-479-744A-23	Sequence 23, Appl	1115	103.5	6.7	598	2	US-09-310-463-13	Sequence 13, Appl
1043	104.5	6.8	309	2	US-08-280-757B-23	Sequence 23, Appl	1116	103.5	6.7	598	2	US-08-842-248A-10	Sequence 10, Appl
1044	104.5	6.8	309	2	US-08-205-657A-21	Sequence 21, Appl	1117	103.5	6.7	615	2	US-08-985-950-18	Sequence 18, Appl
1045	104.5	6.8	309	2	US-08-702-525-21	Sequence 21, Appl	1118	103.5	6.7	615	2	US-08-985-950-18	Sequence 18, Appl
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1047	104.5	6.8	309	2	US-09-651-200-22	Sequence 22, Appl	1120	103.5	6.7	615	2	US-09-546-049-18	Sequence 18, Appl
1048	104.5	6.8	309	2	US-09-657-135-33	Sequence 33, Appl	1121	103	6.7	238	2	US-08-793-450-6	Sequence 6, Appli
1049	104.5	6.8	309	2	US-09-425-762-23	Sequence 23, Appl	1122	103	6.7	282	2	US-10-027-736A-66	Sequence 66, Appl

1123	103	6.7	318	2	US-09-656-952-2	Sequence 2, Appl1	1196	101	6.5	466	1	US-08-432-016-4	Sequence 4, Appl1
1124	103	6.7	344	2	US-09-656-952-19	Sequence 19, Appl1	1197	101	6.5	466	1	US-08-684-594-4	Sequence 4, Appl1
1125	103	6.7	366	2	US-08-875-811-55	Sequence 55, Appl1	1198	101	6.5	475	2	US-09-740-002-25	Sequence 25, Appl1
1126	103	6.7	451	2	US-09-247-352-3	Sequence 3, Appl1	1199	101	6.5	757	2	US-08-434-000A-6	Sequence 6, Appl1
1127	103	6.7	451	2	US-09-466-635-3	Sequence 3, Appl1	1200	101	6.5	757	2	US-09-312-157-6	Sequence 6, Appl1
1128	103	6.7	1474	2	US-09-677-046A-4	Sequence 4, Appl1	1201	101	6.5	757	2	US-09-717-888-6	Sequence 6, Appl1
1129	103	6.7	1503	2	US-09-677-046A-6	Sequence 6, Appl1	1202	101	6.5	900	2	US-10-282-162-40	Sequence 40, Appl1
1130	103	6.7	1509	2	US-09-677-046A-2	Sequence 2, Appl1	1203	101	6.5	902	2	US-10-282-162-42	Sequence 42, Appl1
1131	102.5	6.6	181	2	US-08-753-007A-4	Sequence 4, Appl1	1204	101	6.5	902	2	US-10-282-162-44	Sequence 44, Appl1
1132	102.5	6.6	181	2	US-09-398-496-4	Sequence 4, Appl1	1205	101	6.5	976	2	US-08-750-111A-1	Sequence 1, Appl1
1133	102.5	6.6	271	1	US-08-894-922A-10	Sequence 10, Appl1	1206	101	6.5	1518	2	US-09-487-558B-152	Sequence 15, App
1134	102.5	6.6	284	2	US-09-184-658-40	Sequence 40, Appl1	1207	100.5	6.5	246	1	US-07-843-125-11	Sequence 11, Appl1
1135	102.5	6.6	284	2	US-09-504-262D-40	Sequence 40, Appl1	1208	100.5	6.5	288	2	US-09-651-200-14	Sequence 14, Appl1
1136	102.5	6.6	468	2	US-09-485-737B-67	Sequence 67, Appl1	1209	100.5	6.5	467	2	US-08-030-175-41	Sequence 41, Appl1
1137	102.5	6.6	468	2	US-10-071-485-67	Sequence 67, Appl1	1210	100.5	6.5	467	2	US-08-030-175-42	Sequence 42, Appl1
1138	102.5	6.6	605	2	US-08-753-007A-2	Sequence 2, Appl1	1211	100	6.5	98	2	US-09-270-767-60078	Sequence 60078, A
1139	102.5	6.6	605	2	US-09-398-496-2	Sequence 2, Appl1	1212	100	6.5	201	2	US-08-955-937A-2	Sequence 2, Appl1
1140	102.5	6.6	653	2	US-09-520-781-10	Sequence 2, Appl1	1213	100	6.5	201	2	US-09-300-985-2	Sequence 2, Appl1
1141	102.5	6.6	653	2	US-09-957-187-10	Sequence 10, Appl1	1214	100	6.5	229	1	US-08-887-352B-21	Sequence 21, Appl1
1142	102.5	6.6	653	2	US-09-991-053-10	Sequence 10, Appl1	1215	100	6.5	229	2	US-09-109-207C-21	Sequence 21, Appl1
1143	102.5	6.6	711	2	US-09-485-737B-90	Sequence 90, Appl1	1216	100	6.5	229	2	US-0286-005-21	Sequence 21, Appl1
1144	102.5	6.6	711	2	US-10-071-485-90	Sequence 90, Appl1	1217	100	6.5	229	2	US-09-920-111-21	Sequence 21, Appl1
1145	102	6.6	146	2	US-09-270-767-33187	Sequence 33187, A	1218	100	6.5	229	2	US-09-716-028-21	Sequence 21, Appl1
1146	102	6.6	267	2	US-09-485-737B-2	Sequence 2, Appl1	1219	100	6.5	229	1	US-10-113-996-26	Sequence 26, Appl1
1147	102	6.6	267	2	US-10-071-485-2	Sequence 2, Appl1	1220	100	6.5	233	1	US-08-887-352B-26	Sequence 26, Appl1
1148	102	6.6	296	2	US-09-667-135-36	Sequence 36, Appl1	1221	100	6.5	233	2	US-09-109-207C-26	Sequence 26, Appl1
1149	102	6.6	498	2	US-09-354-151-2	Sequence 2, Appl1	1222	100	6.5	233	2	US-09-296-005-46	Sequence 26, Appl1
1150	102	6.6	728	1	US-07-912-952-4	Sequence 4, Appl1	1223	100	6.5	233	2	US-09-920-111-26	Sequence 26, Appl1
1151	102	6.6	999	1	US-08-252-626A-2	Sequence 2, Appl1	1224	100	6.5	233	2	US-09-716-028-26	Sequence 26, Appl1
1152	102	6.6	999	2	US-09-949-016-6718	Sequence 6718, Ap	1225	100	6.5	233	2	US-10-113-996-26	Sequence 26, Appl1
1153	101.5	6.6	222	2	US-09-698-705-13	Sequence 13, Appl1	1226	100	6.5	268	2	US-09-976-118-1	Sequence 1, Appl1
1154	101.5	6.6	278	2	US-09-570-367C-2	Sequence 2, Appl1	1227	100	6.5	329	2	US-09-651-200-18	Sequence 18, Appl1
1155	101.5	6.6	278	2	US-09-915-524-2	Sequence 2, Appl1	1228	100	6.5	329	2	US-09-303-040-6	Sequence 6, Appl1
1156	101.5	6.6	278	2	US-09-934-634-2	Sequence 2, Appl1	1229	100	6.5	431	2	US-08-646-551-26	Sequence 26, Appl1
1157	101.5	6.6	278	2	US-09-917-278-2	Sequence 2, Appl1	1230	100	6.5	451	1	US-08-887-352B-18	Sequence 18, Appl1
1158	101.5	6.6	297	2	US-09-486-814A-2	Sequence 2, Appl1	1231	100	6.5	451	2	US-09-680-145-2	Sequence 2, Appl1
1159	101.5	6.6	352	2	US-09-203-958A-2	Sequence 2, Appl1	1232	100	6.5	451	2	US-09-109-207C-18	Sequence 18, Appl1
1160	101.5	6.6	410	1	US-08-091-519-13	Sequence 13, Appl1	1233	100	6.5	451	2	US-09-282-505-2	Sequence 2, Appl1
1161	101.5	6.6	410	1	US-08-442-043A-13	Sequence 13, Appl1	1234	100	6.5	451	2	US-09-054-255-2	Sequence 2, Appl1
1162	101.5	6.6	410	2	US-09-173-151A-27	Sequence 27, Appl1	1235	100	6.5	451	2	US-09-296-806-18	Sequence 18, Appl1
1163	101.5	6.6	410	2	US-09-461-908-13	Sequence 13, Appl1	1236	100	6.5	451	2	US-09-680-145-2	Sequence 2, Appl1
1164	101.5	6.6	410	2	US-08-441-893A-13	Sequence 13, Appl1	1237	100	6.5	451	2	US-09-920-171-18	Sequence 18, Appl1
1165	101.5	6.6	410	4	PCT-US91-03478-13	Sequence 13, Appl1	1238	100	6.5	451	2	US-09-716-028-18	Sequence 18, Appl1
1166	101.5	6.6	418	2	US-09-614-912-136	Sequence 8, Appl1	1239	100	6.5	451	2	US-09-483-588-2	Sequence 2, Appl1
1167	101.5	6.6	470	2	US-10-104-047-3730	Sequence 3730, Ap	1240	100	6.5	451	2	US-10-113-996-18	Sequence 18, Appl1
1168	101.5	6.6	478	2	US-08-487-550-8	Sequence 8, Appl1	1241	100	6.5	910	2	US-09-313-942-28	Sequence 28, Appl1
1169	101.5	6.6	478	2	US-09-526-098-8	Sequence 8, Appl1	1242	100	6.5	910	2	US-10-282-162-28	Sequence 28, Appl1
1170	101.5	6.6	478	2	US-09-383-916-8	Sequence 8, Appl1	1243	100	6.4	174	2	US-09-858-664A-26	Sequence 26, Appl1
1171	101.5	6.6	478	2	US-09-758-173-8	Sequence 8, Appl1	1244	99.5	6.4	174	2	US-10-274-978-27	Sequence 27, Appl1
1172	101.5	6.6	478	2	US-09-576-424-8	Sequence 8, Appl1	1245	99.5	6.4	174	2	US-10-697-263-27	Sequence 27, Appl1
1173	101.5	6.6	486	1	US-08-432-016-6	Sequence 6, Appl1	1246	99.5	6.4	259	2	US-10-104-047-2303	Sequence 2303, Ap
1174	101.5	6.6	486	1	US-08-684-594-6	Sequence 6, Appl1	1247	99.5	6.4	339	2	US-09-719-243-2	Sequence 2, Appl1
1175	101.5	6.6	738	6	5264554-2	Patent No. 5264554	1248	99.5	6.4	347	1	US-07-940-861-33	Sequence 43, Appl1
1176	101.5	6.6	945	2	US-10-037-417-38	Sequence 38, Appl1	1249	99.5	6.4	347	1	US-08-459-512-124	Sequence 43, Appl1
1177	101	6.5	241	2	US-09-915-789A-11	Sequence 11, Appl1	1250	99.5	6.4	347	1	US-08-459-657-43	Sequence 43, Appl1
1178	101	6.5	246	1	US-08-553-497A-24	Sequence 24, Appl1	1251	99.5	6.4	347	1	US-08-460-112-43	Sequence 43, Appl1
1179	101	6.5	253	2	US-09-027-449-52	Sequence 52, Appl1	1252	99.5	6.4	347	2	US-08-466-465-8	Sequence 8, Appl1
1180	101	6.5	253	2	US-08-804-444A-52	Sequence 52, Appl1	1253	99.5	6.4	347	2	US-09-730-465-8	Sequence 43, Appl1
1181	101	6.5	253	2	US-09-026-985-52	Sequence 52, Appl1	1254	99.5	6.4	347	4	PCT-US92-02050-43	Sequence 43, Appl1
1182	101	6.5	253	2	US-09-121-952A-52	Sequence 52, Appl1	1255	99.5	6.4	409	2	US-09-075-215A-17	Sequence 17, Appl1
1183	101	6.5	253	2	US-09-234-340A-52	Sequence 52, Appl1	1256	99.5	6.4	452	2	US-09-773-877B-16	Sequence 16, Appl1
1184	101	6.5	253	2	US-09-335-014-52	Sequence 52, Appl1	1257	99	6.4	229	1	US-08-887-352B-20	Sequence 20, Appl1
1185	101	6.5	256	2	US-09-027-449-70	Sequence 70, Appl1	1258	99	6.4	229	2	US-09-109-207C-20	Sequence 20, Appl1
1186	101	6.5	256	2	US-09-026-985-70	Sequence 70, Appl1	1259	99	6.4	229	2	US-09-296-005-20	Sequence 20, Appl1
1187	101	6.5	256	2	US-09-121-952A-70	Sequence 70, Appl1	1260	99	6.4	229	2	US-09-920-171-20	Sequence 20, Appl1
1188	101	6.5	256	2	US-09-234-340A-70	Sequence 70, Appl1	1261	99	6.4	229	2	US-09-716-028-20	Sequence 20, Appl1
1189	101	6.5	256	2	US-09-355-014-70	Sequence 70, Appl1	1262	99	6.4	229	1	US-10-113-996-20	Sequence 20, Appl1
1190	101	6.5	298	2	US-09-027-449-60	Sequence 60, Appl1	1263	99	6.4	233	1	US-08-887-352B-25	Sequence 25, Appl1
1191	101	6.5	298	2	US-08-804-444A-60	Sequence 60, Appl1	1264	99	6.4	233	2	US-09-109-207C-25	Sequence 25, Appl1
1192	101	6.5	298	2	US-09-026-985-60	Sequence 60, Appl1	1265	99	6.4	233	2	US-09-296-005-25	Sequence 25, Appl1
1193	101	6.5	298	2	US-09-121-952A-60	Sequence 60, Appl1	1266	99	6.4	233	2	US-09-920-171-25	Sequence 25, Appl1
1194	101	6.5	298	2	US-09-234-340A-60	Sequence 60, Appl1	1267	99	6.4	233	2	US-09-716-028-25	Sequence 25, Appl1
1195	101	6.5	298	2	US-09-355-014-60	Sequence 60, Appl1	1268	99	6.4	233	2	US-10-113-996-25	Sequence 25, Appl1

1269	99	6.4	240	1	US-08-956-047-25	Sequence 25, Appl	1342	96.5	6.2	245	2	US-08-918-148-78	Sequence 78, Appl
1270	99	6.4	451	1	US-08-887-352B-14	Sequence 14, Appl	1343	96.5	6.2	263	1	US-08-752-844-66	Sequence 66, Appl
1271	99	6.4	451	1	US-08-887-352B-16	Sequence 16, Appl	1344	96.5	6.2	263	1	US-09-293-533-66	Sequence 66, Appl
1272	99	6.4	451	2	US-08-466-151-65	Sequence 65, Appl	1345	96.5	6.2	278	2	US-09-570-367C-21	Sequence 21, Appl
1273	99	6.4	451	2	US-09-109-207C-14	Sequence 14, Appl	1346	96.5	6.2	278	2	US-09-915-524-21	Sequence 21, Appl
1274	99	6.4	451	2	US-09-109-207C-16	Sequence 16, Appl	1347	96.5	6.2	278	2	US-09-934-634-21	Sequence 21, Appl
1275	99	6.4	451	2	US-09-296-005-14	Sequence 14, Appl	1348	96.5	6.2	278	2	US-09-917-278-21	Sequence 21, Appl
1276	99	6.4	451	2	US-09-296-005-16	Sequence 16, Appl	1349	96.5	6.2	283	1	US-08-332-562A-136	Sequence 136, App
1277	99	6.4	451	2	US-09-920-171-14	Sequence 14, Appl	1350	96.5	6.2	288	1	US-08-147-772-2	Sequence 2, Appl1
1278	99	6.4	451	2	US-09-920-171-16	Sequence 16, Appl	1351	96.5	6.2	288	1	US-08-456-104-6	Sequence 6, Appl1
1279	99	6.4	451	2	US-09-716-028-14	Sequence 14, Appl	1352	96.5	6.2	288	1	US-08-101-624-23	Sequence 23, Appl
1280	99	6.4	451	2	US-09-716-028-16	Sequence 16, Appl	1353	96.5	6.2	288	1	US-08-751-767A-6	Sequence 6, Appl1
1281	99	6.4	451	2	US-10-113-996-14	Sequence 14, Appl	1354	96.5	6.2	288	1	US-08-153-262-2	Sequence 2, Appl1
1282	99	6.4	451	2	US-10-113-996-16	Sequence 16, Appl	1355	96.5	6.2	288	2	US-08-479-144A-29	Sequence 29, Appl
1283	99	6.4	451	2	US-09-925-179-65	Sequence 65, Appl	1356	96.5	6.2	288	2	US-08-280-757B-29	Sequence 29, Appl
1284	99	6.4	451	2	US-09-925-179-66	Sequence 66, Appl	1357	96.5	6.2	288	2	US-09-159-135-2	Sequence 2, Appl1
1285	99	6.4	461	1	US-08-463-587A-26	Sequence 26, Appl	1358	96.5	6.2	288	2	US-08-205-697A-19	Sequence 19, Appl
1286	99	6.4	461	1	US-08-463-667A-4	Sequence 4, Appl1	1359	96.5	6.2	288	2	US-08-702-525-19	Sequence 19, Appl
1287	99	6.4	461	2	US-08-923-854-26	Sequence 26, Appl	1360	96.5	6.2	288	2	US-09-450-798-2	Sequence 2, Appl1
1288	99	6.4	461	4	PCT-US91-09133-27	Sequence 27, Appl	1361	96.5	6.2	288	2	US-08-403-253A-2	Sequence 2, Appl1
1289	99	6.4	825	1	US-07-912-952-2	Sequence 2, Appl	1362	96.5	6.2	288	2	US-09-651-200-13	Sequence 13, Appl
1290	99	6.4	238	1	US-08-162-809-16	Sequence 16, Appl	1363	96.5	6.2	288	2	US-09-667-135-34	Sequence 34, Appl
1291	98.5	6.4	238	1	US-09-949-016-11628	Sequence 11628, A	1364	96.5	6.2	288	2	US-08-435-816-12	Sequence 2, Appl1
1292	98.5	6.4	246	1	US-08-469-486-57	Sequence 57, Appl	1365	96.5	6.2	288	2	US-09-425-762-29	Sequence 29, Appl
1293	98.5	6.4	246	1	US-08-469-658-57	Sequence 57, Appl	1366	96.5	6.2	288	2	US-09-837-867A-19	Sequence 19, Appl
1294	98.5	6.4	260	2	US-09-910-059-93	Sequence 93, Appl	1367	96.5	6.2	288	2	US-09-910-174B-5	Sequence 5, Appl1
1295	98.5	6.4	260	2	US-08-564-164A-4	Sequence 4, Appl	1368	96.5	6.2	288	2	US-09-620-661-5	Sequence 5, Appl1
1296	98.5	6.4	264	2	US-08-564-164A-4	Sequence 4, Appl	1369	96.5	6.2	288	2	US-08-453-386A-2	Sequence 2, Appl1
1297	98.5	6.4	306	2	US-09-171-945-95	Sequence 95, Appl	1370	96.5	6.2	288	2	US-09-206-132-6	Sequence 6, Appl1
1298	98.5	6.4	306	2	US-09-910-059-95	Sequence 95, Appl	1371	96.5	6.2	288	2	US-09-425-516-29	Sequence 29, Appl
1299	98.5	6.4	334	2	US-09-197-970B-7	Sequence 7, Appl1	1372	96.5	6.2	288	2	US-09-350-202-2	Sequence 2, Appl1
1300	98.5	6.4	440	2	US-09-866-028-61	Sequence 61, Appl	1373	96.5	6.2	288	2	US-09-915-789A-15	Sequence 15, Appl
1301	98.5	6.4	440	2	US-09-944-457-61	Sequence 61, Appl	1374	96.5	6.2	288	2	US-08-592-711-2	Sequence 2, Appl1
1302	98.5	6.4	440	2	US-09-945-584-61	Sequence 61, Appl	1375	96.5	6.2	288	2	US-09-349-915B-2	GENERAL INFORMA
1303	98.5	6.4	440	2	US-09-944-944-61	Sequence 61, Appl	1376	96.5	6.2	288	4	PCT-US95-02576-19	Sequence 19, Appl
1304	98.5	6.4	440	2	US-09-945-587-61	Sequence 61, Appl	1377	96.5	6.2	449	1	US-08-458-816-13	Sequence 13, Appl
1305	98.5	6.4	442	2	US-09-778-510-20	Sequence 20, Appl	1378	96.5	6.2	969	2	US-09-949-016-8059	Sequence 8059, Ap
1306	98.5	6.4	442	2	US-09-930-803-1	Sequence 1, Appl1	1379	96.5	6.2	2864	2	US-08-469-260A-394	Sequence 394, App
1307	98.5	6.4	442	2	US-10-104-047-812	Sequence 3812, Ap	1380	96.5	6.2	2864	2	US-08-488-446-394	Sequence 394, App
1308	98.5	6.4	613	2	US-09-171-945-113	Sequence 113, App	1381	96.5	6.2	2864	2	US-08-457-344A-394	Sequence 394, App
1309	98.5	6.4	613	2	US-09-910-059-113	Sequence 113, App	1382	96.5	6.2	2864	2	US-08-424-550B-394	Sequence 394, App
1310	98.5	6.4	716	2	US-09-171-945-125	Sequence 125, App	1383	96.5	6.2	139	1	US-08-182-067-10	Sequence 10, Appl
1311	98.5	6.4	716	2	US-09-910-059-125	Sequence 125, App	1384	96.5	6.2	139	1	US-08-465-313-10	Sequence 10, Appl
1312	98.5	6.4	832	2	US-08-630-820-7	Sequence 7, Appl1	1385	96.5	6.2	139	2	US-09-809-739-5	Sequence 5, Appl1
1313	98.5	6.4	832	2	US-09-273-453-7	Sequence 7, Appl1	1386	96.5	6.2	139	2	US-09-378-967-10	Sequence 10, Appl
1314	98	6.3	239	1	US-08-353-400-37	Sequence 37, Appl	1387	96.5	6.2	155	1	US-08-494-577-6	Sequence 6, Appl1
1315	98	6.3	309	2	US-09-079-029-9	Sequence 9, Appl1	1388	96.5	6.2	155	1	US-08-494-577-7	Sequence 7, Appl1
1316	98	6.3	451	2	US-09-925-179-68	Sequence 68, Appl	1389	96.5	6.2	155	1	US-08-795-868-6	Sequence 6, Appl1
1317	98	6.3	460	2	US-10-630-406-5	Sequence 5, Appl1	1390	96.5	6.2	155	1	US-08-795-868-7	Sequence 7, Appl1
1318	98	6.3	513	2	US-09-910-174B-18	Sequence 18, Appl	1391	96.5	6.2	155	2	US-09-303-069-6	Sequence 6, Appl1
1319	98	6.3	513	2	US-09-620-461-18	Sequence 18, Appl	1392	96.5	6.2	155	2	US-09-103-069-7	Sequence 7, Appl1
1320	98	6.3	668	2	US-09-751-389-6	Sequence 6, Appl1	1393	96.5	6.2	155	2	US-09-134-250-6	Sequence 6, Appl1
1321	98	6.3	1123	2	US-09-949-016-6230	Sequence 6230, Ap	1394	96.5	6.2	155	2	US-09-833-350-7	Sequence 7, Appl1
1322	98	6.3	1128	2	US-09-949-016-7522	Sequence 7522, Ap	1395	96.5	6.2	222	2	US-09-893-737-108	Sequence 108, Appl
1323	97.5	6.3	236	2	US-09-698-705-10	Sequence 10, Appl	1396	96.5	6.2	250	2	US-10-194-975-110	Sequence 110, App
1324	97.5	6.3	266	2	US-09-746-311B-114	Sequence 114, App	1397	96.5	6.2	261	2	US-09-270-767-32898	Sequence 32898, A
1325	97.5	6.3	293	6	5189147-3	Patent No. 5189147	1398	96.5	6.2	261	2	US-09-270-767-48115	Sequence 48115, A
1326	97.5	6.3	353	2	US-09-203-958A-4	Sequence 4, Appl1	1399	96.5	6.2	266	6	5175384-11	Patent No. 5175384
1327	97.5	6.3	1241	2	US-09-040-774-2	Sequence 2, Appl1	1400	96.5	6.2	495	2	US-09-948-004-18	Sequence 18, Appl
1328	97	6.3	330	1	US-08-332-562A-81	Sequence 81, Appl	1401	96.5	6.2	582	2	US-09-702-705-334	Sequence 334, App
1329	97	6.3	330	1	US-08-332-562A-134	Sequence 134, App	1402	96.5	6.2	582	2	US-09-726-457-334	Sequence 334, App
1330	97	6.3	365	2	US-08-875-811-53	Sequence 53, Appl	1403	96.5	6.2	582	2	US-09-614-124B-334	Sequence 334, App
1331	97	6.3	482	2	US-09-508-031-16	Sequence 16, Appl	1404	96.5	6.2	582	2	US-09-611-325-334	Sequence 334, App
1332	97	6.3	541	2	US-09-485-737B-85	Sequence 85, Appl	1405	96.5	6.2	582	2	US-09-589-184-334	Sequence 334, App
1333	97	6.3	541	2	US-10-071-485-85	Sequence 85, Appl	1406	96.5	6.2	582	2	US-09-688-824-334	Sequence 334, App
1334	97	6.3	581	1	US-08-724-394A-2	Sequence 2, Appl1	1407	96.5	6.2	582	2	US-10-017-754-334	Sequence 334, App
1335	97	6.3	789	2	US-09-831-846-2	Sequence 2, Appl1	1408	96.5	6.2	582	2	US-09-651-563-334	Sequence 334, App
1336	96.5	6.2	222	1	US-08-458-516-32	Sequence 22, Appl	1409	96.5	6.2	582	2	US-09-519-642-334	Sequence 334, App
1337	96.5	6.2	235	1	US-08-458-516-33	Sequence 23, Appl	1410	96.5	6.2	583	1	US-08-432-016-2	Sequence 2, Appl1
1338	96.5	6.2	240	2	US-09-485-737B-91	Sequence 91, Appl	1411	96.5	6.2	583	1	US-08-684-594-2	Sequence 2, Appl1
1339	96.5	6.2	240	2	US-10-071-485-91	Sequence 91, Appl	1412	96.5	6.2	604	1	US-09-949-016-9548	Sequence 9548, Ap
1340	96.5	6.2	244	2	US-09-244-369B-1	Sequence 1, Appl1	1413	95.5	6.2	232	1	US-08-425-763-2	Sequence 2, Appl1
1341	96.5	6.2	244	2	US-09-940-391-1	Sequence 1, Appl1	1414	95.5	6.2	232	2	US-08-811-757-2	Sequence 2, Appl1

1415	95.5	6.2	222	2	US-09-249-230-2	Sequence 2, Appl1	1488	94.5	6.1	270	2	US-09-976-118-2	Sequence 2, Appl1
1416	95.5	6.2	225	2	US-09-049-672A-12	Sequence 12, Appl	1489	94.5	6.1	313	2	US-09-756-983-15	Sequence 15, Appl
1417	95.5	6.2	232	1	US-08-398-612A-56	Sequence 56, Appl	1490	94.5	6.1	360	2	US-09-949-016-8370	Sequence 8370, Ap
1418	95.5	6.2	242	1	US-08-398-612A-56	Sequence 56, Appl	1491	94.5	6.1	432	2	US-08-477-4608-2	Sequence 2, Appl1
1419	95.5	6.2	242	1	US-08-398-611A-55	Sequence 56, Appl	1492	94.5	6.1	432	2	US-08-379-516-2	Sequence 2, Appl1
1420	95.5	6.2	242	1	US-08-491-334A-56	Sequence 56, Appl	1493	94.5	6.1	432	2	US-09-329-916-2	Sequence 2, Appl1
1421	95.5	6.2	242	2	US-09-027-449-42	Sequence 42, Appl	1494	94.5	6.1	432	2	US-08-465-372A-2	Sequence 2, Appl1
1422	95.5	6.2	242	2	US-08-804-444A-42	Sequence 42, Appl	1495	94.5	6.1	432	2	US-09-409-006A-2	Sequence 2, Appl1
1423	95.5	6.2	242	2	US-09-026-985-42	Sequence 42, Appl	1496	94.5	6.1	432	2	US-08-484-681-2	Sequence 2, Appl1
1424	95.5	6.2	242	2	US-09-121-952A-42	Sequence 42, Appl	1497	94.5	6.1	432	2	US-09-766-995-2	Sequence 2, Appl1
1425	95.5	6.2	242	2	US-09-334-340A-42	Sequence 42, Appl	1498	94.5	6.1	432	4	PCT-US93-07422-2	Sequence 2, Appl1
1426	95.5	6.2	242	2	US-09-355-014-42	Sequence 42, Appl	1499	94.5	6.1	467	1	US-08-704-744-01	Sequence 81, Appl
1427	95.5	6.2	257	2	US-08-411-295F-78	Sequence 78, Appl	1500	94.5	6.1	557	2	US-09-773-877B-14	Sequence 14, Appl
1428	95.5	6.2	258	1	US-08-860-174A-13	Sequence 13, Appl	ALIGNMENTS						
1429	95.5	6.2	310	2	US-09-079-029-11	Sequence 11, Appl	RESULT 1						
1430	95.5	6.2	423	2	US-09-778-510-22	Sequence 22, Appl	US-09-188-930-331						
1431	95.5	6.2	462	2	US-09-773-877B-18	Sequence 18, Appl	Sequence 331, Application US/09188930A						
1432	95.5	6.2	474	2	US-09-848-832-3	Sequence 3, Appl1	Patent No. 6150502						
1433	95.5	6.2	504	2	US-09-270-767-43244	Sequence 43244, A	GENERAL INFORMATION:						
1434	95.5	6.2	581	2	US-09-499-522-18	Sequence 18, Appl	APPLICANT: Watson, James D.						
1435	95.5	6.2	581	2	US-09-269-939A-12	Sequence 12, Appl	APPLICANT: Strachan, Lorna						
1436	95.5	6.2	782	2	US-09-813-290-4	Sequence 4, Appl1	APPLICANT: Sleeman, Matthew						
1437	95.5	6.2	875	2	US-09-813-290-2	Sequence 4, Appl1	APPLICANT: Onrust, Rene						
1438	95.5	6.2	945	2	US-10-037-417-121	Sequence 121, App	APPLICANT: Murison, James Greg						
1439	95	6.2	92	6	5284931-8	Patent No. 5284931	TITLE OF INVENTION: Compositions Isolated From Skin Cells						
1440	95	6.2	139	1	US-08-039-198B-10	Sequence 10, Appl	TITLE OF INVENTION: and Methods For Their Use						
1441	95	6.2	212	4	PCT-US95-02576-63	Sequence 63, Appl	FILE REFERENCE: 11000.1011c1						
1442	95	6.2	225	2	US-09-456-090A-98	Sequence 98, Appl	CURRENT FILING DATE: 1998-11-09						
1443	95	6.2	225	2	US-09-453-234-98	Sequence 98, Appl	NUMBER OF SEQ ID NOS: 348						
1444	95	6.2	225	2	US-08-702-525-65	Sequence 65, Appl	SOFTWARE: FastSeq for Windows Version 3.0						
1445	95	6.2	226	2	US-09-915-789A-21	Sequence 21, Appl	SEQ ID NO 331						
1446	95	6.2	226	2	PCT-US95-02576-65	Sequence 65, Appl	LENGTH: 299						
1447	95	6.2	226	4	PCT-US95-02576-65	Sequence 65, Appl	TYPE: PRT						
1448	95	6.2	225	2	US-09-485-737B-93	Sequence 93, Appl	ORGANISM: Human						
1449	95	6.2	225	2	US-10-071-485-93	Sequence 93, Appl	US-09-188-930-331						
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1453	95	6.2	421	1	US-07-934-373C-22	Sequence 22, Appl	100.0%; Score 1544; DB 2; Length 299;						
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1459	95	6.2	421	1	US-08-437-642B-22	Sequence 22, Appl	100.0%; Score 1544; DB 2; Length 299;						
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1465	95	6.2	421	1	US-08-437-642B-22	Sequence 22, Appl	100.0%; Score 1544; DB 2; Length 299;						
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1468	95	6.2	421	1	US-08-437-642B-22	Sequence 22, Appl	100.0%; Score 1544; DB 2; Length 299;						
1469	95	6.2	421	1	US-08-437-642B-22	Sequence 22, Appl	Beat Local Similarity 100.0%; Pident. No. 8.3e-135;						
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1471	95	6.2	421	1	US-08-437-642B-22	Sequence 22, Appl	100.0%; Score 1544; DB 2; Length 299;						
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TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-70150US
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 299
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-462-270-2

No. 299
For 100% date

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAKYERKLLCLFILAAILLCSLALGSVTVHSEPEVRIPENNPKVLSGAYSGFSSPRV 60
DB 1 MGTAKYERKLLCLFILAAILLCSLALGSVTVHSEPEVRIPENNPKVLSGAYSGFSSPRV 60
QY 61 EWMFDGDDTTRLVCYNNKKTASYEDRVTFPLPTITKSVTRDTGTYTCMVSEEGNSYG 120
DB 61 EWMFDGDDTTRLVCYNNKKTASYEDRVTFPLPTITKSVTRDTGTYTCMVSEEGNSYG 120
QY 121 EVVKYKLVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTFKDGIVMPTNPKST 180
DB 121 EVVKYKLVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTFKDGIVMPTNPKST 180
QY 181 RAFTNSSYVLPNTTGGELVFDPLASDTGEYSCEARNYGTPTMTSNAVRMEAVERNVGIY 240
DB 181 RAFTNSSYVLPNTTGGELVFDPLASDTGEYSCEARNYGTPTMTSNAVRMEAVERNVGIY 240
QY 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKGTSKKVIYQPSARSEGEFKQTSFLV 299
DB 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKGTSKKVIYQPSARSEGEFKQTSFLV 299

RESULT 3
US-09-254-465A-1
Sequence 1, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Aemkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 1
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match 100.0%; Score 1544; DB 2; Length 299;

Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAKYERKLLCLFILAAILLCSLALGSVTVHSEPEVRIPENNPKVLSGAYSGFSSPRV 60
DB 1 MGTAKYERKLLCLFILAAILLCSLALGSVTVHSEPEVRIPENNPKVLSGAYSGFSSPRV 60
QY 61 EWMFDGDDTTRLVCYNNKKTASYEDRVTFPLPTITKSVTRDTGTYTCMVSEEGNSYG 120
DB 61 EWMFDGDDTTRLVCYNNKKTASYEDRVTFPLPTITKSVTRDTGTYTCMVSEEGNSYG 120
QY 121 EVVKYKLVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTFKDGIVMPTNPKST 180
DB 121 EVVKYKLVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTFKDGIVMPTNPKST 180
QY 181 RAFTNSSYVLPNTTGGELVFDPLASDTGEYSCEARNYGTPTMTSNAVRMEAVERNVGIY 240
DB 181 RAFTNSSYVLPNTTGGELVFDPLASDTGEYSCEARNYGTPTMTSNAVRMEAVERNVGIY 240
QY 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKGTSKKVIYQPSARSEGEFKQTSFLV 299
DB 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKGTSKKVIYQPSARSEGEFKQTSFLV 299

RESULT 4
US-09-312-283C-189
Sequence 189, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ormrod, Rene
APPLICANT: Morrison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 189
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-189

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAKYERKLLCLFILAAILLCSLALGSVTVHSEPEVRIPENNPKVLSGAYSGFSSPRV 60
DB 1 MGTAKYERKLLCLFILAAILLCSLALGSVTVHSEPEVRIPENNPKVLSGAYSGFSSPRV 60
QY 61 EWMFDGDDTTRLVCYNNKKTASYEDRVTFPLPTITKSVTRDTGTYTCMVSEEGNSYG 120
DB 61 EWMFDGDDTTRLVCYNNKKTASYEDRVTFPLPTITKSVTRDTGTYTCMVSEEGNSYG 120
QY 121 EVVKYKLVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTFKDGIVMPTNPKST 180
DB 121 EVVKYKLVLPSPKPTVINIPSSATIGNRAVLTCSEODGSPSEYTFKDGIVMPTNPKST 180
QY 181 RAFTNSSYVLPNTTGGELVFDPLASDTGEYSCEARNYGTPTMTSNAVRMEAVERNVGIY 240
DB 181 RAFTNSSYVLPNTTGGELVFDPLASDTGEYSCEARNYGTPTMTSNAVRMEAVERNVGIY 240
QY 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKGTSKKVIYQPSARSEGEFKQTSFLV 299
DB 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKGTSKKVIYQPSARSEGEFKQTSFLV 299

```
RESULT 5
US-09-312-283C-331
; Sequence 331, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011C2
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-331

Query Match      100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGTQAVERKLCFLFLAILLCSLALGVTYSSSEPVRIPENNPVKLSGAYSGFSSPRV 60
DB      1  MGTQAVERKLCFLFLAILLCSLALGVTYSSSEPVRIPENNPVKLSGAYSGFSSPRV 60
QY      61  EKKPDGDTTRLVCCYNNKITASYEDRVTFLEPTGITFKSVTREDDTGYTCMVSEEGNSYG 120
DB      61  EKKPDGDTTRLVCCYNNKITASYEDRVTFLEPTGITFKSVTREDDTGYTCMVSEEGNSYG 120
QY      121  EVKVKLIYLVPPSKPTVNISSATIGNRAVLTCSQDQSPSEYTWFKDGIYMPNPKST 180
DB      121  EVKVKLIYLVPPSKPTVNISSATIGNRAVLTCSQDQSPSEYTWFKDGIYMPNPKST 180
QY      181  RAFSNSYVLNPTTGELVFDPLSASDTGEYSCAANGVGTPTMTSNAVMEAVERRVGYIV 240
DB      181  RAFSNSYVLNPTTGELVFDPLSASDTGEYSCAANGVGTPTMTSNAVMEAVERRVGYIV 240
QY      241  AAVLVTLILGLIVGIMFAYSRGHFDRTKKGTSSKVIYISQPSARSEGEFKQTSSFLV 299
DB      241  AAVLVTLILGLIVGIMFAYSRGHFDRTKKGTSSKVIYISQPSARSEGEFKQTSSFLV 299

RESULT 6
US-09-907-794A-119
; Sequence 119, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlstein, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macner, Jennie P.
; APPLICANT: Pan, James
```

```
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-119

Query Match      100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGTQAVERKLCFLFLAILLCSLALGVTYSSSEPVRIPENNPVKLSGAYSGFSSPRV 60
DB      1  MGTQAVERKLCFLFLAILLCSLALGVTYSSSEPVRIPENNPVKLSGAYSGFSSPRV 60
QY      61  EKKPDGDTTRLVCCYNNKITASYEDRVTFLEPTGITFKSVTREDDTGYTCMVSEEGNSYG 120
DB      61  EKKPDGDTTRLVCCYNNKITASYEDRVTFLEPTGITFKSVTREDDTGYTCMVSEEGNSYG 120
QY      121  EVKVKLIYLVPPSKPTVNISSATIGNRAVLTCSQDQSPSEYTWFKDGIYMPNPKST 180
DB      121  EVKVKLIYLVPPSKPTVNISSATIGNRAVLTCSQDQSPSEYTWFKDGIYMPNPKST 180
QY      181  RAFSNSYVLNPTTGELVFDPLSASDTGEYSCAANGVGTPTMTSNAVMEAVERRVGYIV 240
DB      181  RAFSNSYVLNPTTGELVFDPLSASDTGEYSCAANGVGTPTMTSNAVMEAVERRVGYIV 240
QY      241  AAVLVTLILGLIVGIMFAYSRGHFDRTKKGTSSKVIYISQPSARSEGEFKQTSSFLV 299
DB      241  AAVLVTLILGLIVGIMFAYSRGHFDRTKKGTSSKVIYISQPSARSEGEFKQTSSFLV 299
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Db 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYQPSARSGEFGKQTSSFLV 299

RESULT 7
US-09-905-125A-119
Sequence 119, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A. Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-119
Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8, 3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTRQYERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
DB 1 MGTQAYERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
QY 61 EWKFDGDTTRLYCYNNKKTASVEDRVTPLPTGTTKSYTREDTGYTCVSEGGNSYG 120
DB 61 EWKFDGDTTRLYCYNNKKTASVEDRVTPLPTGTTKSYTREDTGYTCVSEGGNSYG 120
QY 121 EVKVKLIVLPSPKPTVNIIPSSATTIGNRAVLTCSEDDGSPSEYTPKQGIWPTNPKST 180
DB 121 EVKVKLIVLPSPKPTVNIIPSSATTIGNRAVLTCSEDDGSPSEYTPKQGIWPTNPKST 180
QY 181 RAFSNSYVLPPTTGBLVPDPLSADTGEYSCEARNGYGTPTMTSNVRAVERNVGIY 240
DB 181 RAFSNSYVLPPTTGBLVPDPLSADTGEYSCEARNGYGTPTMTSNVRAVERNVGIY 240
QY 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYQSASASEGFKQTSSFLV 299
DB 241 AAVLVTLILGLIVFGIWFAYSRGHFDRTKKGTSSKKVIYQSASASEGFKQTSSFLV 299

RESULT 8
US-09-902-775A-119
Sequence 119, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A. Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-119

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;

Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAQVERKLLCFILAILLCSIALGSAVTYHSSSEPRRIENNPKVLSGASGSPSRV 60
DB 1 MGTAQVERKLLCFILAILLCSIALGSAVTYHSSSEPRRIENNPKVLSGASGSPSRV 60
QY 61 EMKFDQGGTTLVVCYNNKITASYEDRVTFPTGITFKSVTRDGTTCWVSEEGNSYG 120
DB 61 EMKFDQGGTTLVVCYNNKITASYEDRVTFPTGITFKSVTRDGTTCWVSEEGNSYG 120
QY 121 EVKVKLIVLPSPSKPTVINISSATIGNRAVLTCSBQDSSPSEYTWFKDGIWMPNPKST 180
DB 121 EVKVKLIVLPSPSKPTVINISSATIGNRAVLTCSBQDSSPSEYTWFKDGIWMPNPKST 180
QY 181 RAFSNSSVYLNPTTGGELVFPDLSADTGEYSCEARNGYGTMTNSAAMEAVERNVGIY 240
DB 181 RAFSNSSVYLNPTTGGELVFPDLSADTGEYSCEARNGYGTMTNSAAMEAVERNVGIY 240
QY 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKKGTSSKVIYQPSARSGEFKQTSSFLV 299
DB 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKKGTSSKVIYQPSARSGEFKQTSSFLV 299

RESULT 9

US-09-397-243D-3
Sequence 3, Application US/09397243D
Patent No. 6699688
GENERAL INFORMATION:
APPLICANT: Kornecki, Elizabeth
APPLICANT: Sobocka, Maigorzata B.
TITLE OF INVENTION: Human Platelet P11 Receptor
FILE REFERENCE: 011.00221
CURRENT APPLICATION NUMBER: US/09/397,243D
CURRENT FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16

NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-397-243D-3

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;

Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAQVERKLLCFILAILLCSIALGSAVTYHSSSEPRRIENNPKVLSGASGSPSRV 60
DB 1 MGTAQVERKLLCFILAILLCSIALGSAVTYHSSSEPRRIENNPKVLSGASGSPSRV 60
QY 61 EMKFDQGGTTLVVCYNNKITASYEDRVTFPTGITFKSVTRDGTTCWVSEEGNSYG 120
DB 61 EMKFDQGGTTLVVCYNNKITASYEDRVTFPTGITFKSVTRDGTTCWVSEEGNSYG 120
QY 121 EVKVKLIVLPSPSKPTVINISSATIGNRAVLTCSBQDSSPSEYTWFKDGIWMPNPKST 180
DB 121 EVKVKLIVLPSPSKPTVINISSATIGNRAVLTCSBQDSSPSEYTWFKDGIWMPNPKST 180
QY 181 RAFSNSSVYLNPTTGGELVFPDLSADTGEYSCEARNGYGTMTNSAAMEAVERNVGIY 240
DB 181 RAFSNSSVYLNPTTGGELVFPDLSADTGEYSCEARNGYGTMTNSAAMEAVERNVGIY 240
QY 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKKGTSSKVIYQPSARSGEFKQTSSFLV 299
DB 241 AAVLVTLILGILVFGIWFAYSRGHFDRTKKGTSSKVIYQPSARSGEFKQTSSFLV 299

RESULT 10

US-09-906-700-119

Sequence 119, Application US/09906700
Patent No. 6723535

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary B.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698

;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 119
;; LENGTH: 299
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-906-700-119

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTKAQVERKLLCLFLAILLCSIALGSGVTVHSSSEPRVLPENNPVXLSCAYSGFSSPRV 60
DB 1 MGTKAQVERKLLCLFLAILLCSIALGSGVTVHSSSEPRVLPENNPVXLSCAYSGFSSPRV 60
QY 61 EMKFDGDDTTRLVCYNNKITA SYEDRTFLPTGITTFKSVTRDGTGTYTCMVSEGGNSYG 120
DB 61 EMKFDGDDTTRLVCYNNKITA SYEDRTFLPTGITTFKSVTRDGTGTYTCMVSEGGNSYG 120
QY 121 EVVKLILVLPSPKPTYNISSATIGNRAVLTCSEODGSPSEXTYTFKDGIVMPTNPKST 180
DB 121 EVVKLILVLPSPKPTYNISSATIGNRAVLTCSEODGSPSEXTYTFKDGIVMPTNPKST 180
QY 181 RAESNSSYVLPPTTGLVFPDPLSASDTGEYSCEARNGYGTGMTSNVMEAVERNVGIY 240
DB 181 RAESNSSYVLPPTTGLVFPDPLSASDTGEYSCEARNGYGTGMTSNVMEAVERNVGIY 240
QY 241 AAVLVLTLLGLIVFGIWFAYSRGHFRTKKGTSSKKVYISQSPARSEGEFKQTSSFLV 299
DB 241 AAVLVLTLLGLIVFGIWFAYSRGHFRTKKGTSSKKVYISQSPARSEGEFKQTSSFLV 299

RESULT 11
US-09-903-603A-119
; Sequence 119, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Aekhenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Geritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gunney, Austin L.
;; APPLICANT: Hillen, Kenneth, J.
;; APPLICANT: Kijaviri, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tuma, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: GNE 1618P2C12
;; CURRENT FILING DATE: 2001-07-11
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 119
;; LENGTH: 299
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-903-603A-119

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTKAQVERKLLCLFLAILLCSIALGSGVTVHSSSEPRVLPENNPVXLSCAYSGFSSPRV 60
DB 1 MGTKAQVERKLLCLFLAILLCSIALGSGVTVHSSSEPRVLPENNPVXLSCAYSGFSSPRV 60
QY 61 EMKFDGDDTTRLVCYNNKITA SYEDRTFLPTGITTFKSVTRDGTGTYTCMVSEGGNSYG 120

Db 61 EMKFDGDTTRLVYCNKKTASYEDRTFLPTGITFSVREDTGTTCWSEEGNSYG 120
Qy 121 EVKVKLIIVLPSPKPTNIPSSATIGNRAVLTCEODGSPSEYTWKDGIVMPTNPKST 180
Db 121 EVKVKLIIVLPSPKPTNIPSSATIGNRAVLTCEODGSPSEYTWKDGIVMPTNPKST 180
Qy 181 RAPSNSSYVNPPTTGGELVFPDPLSDTGEYSCEARNNGYTPMTSNAVRMEAVERNVGIY 240
Db 181 RAPSNSSYVNPPTTGGELVFPDPLSDTGEYSCEARNNGYTPMTSNAVRMEAVERNVGIY 240
Qy 241 AAVLVTLILGLIVFGIMFAYSRGHPDRTKKTSSKKVIYSQPSARSEGEFKOTSSFLV 299
Db 241 AAVLVTLILGLIVFGIMFAYSRGHPDRTKKTSSKKVIYSQPSARSEGEFKOTSSFLV 299

RESULT 12
US-09-904-920A-119
; Sequence 119, Application US/09904920A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanpeter
; APPLICANT: Gettisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-119

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGTKAVERKLCIFILAILCSIALGQSVTHSEPEVRIPENNPKLSAYSGFSSPRV 60
Qy 61 EMKFDGDTTRLVYCNKKTASYEDRTFLPTGITFSVREDTGTTCWSEEGNSYG 120
Db 61 EMKFDGDTTRLVYCNKKTASYEDRTFLPTGITFSVREDTGTTCWSEEGNSYG 120
Qy 121 EVKVKLIIVLPSPKPTNIPSSATIGNRAVLTCEODGSPSEYTWKDGIVMPTNPKST 180
Db 121 EVKVKLIIVLPSPKPTNIPSSATIGNRAVLTCEODGSPSEYTWKDGIVMPTNPKST 180
Qy 181 RAPSNSSYVNPPTTGGELVFPDPLSDTGEYSCEARNNGYTPMTSNAVRMEAVERNVGIY 240
Db 181 RAPSNSSYVNPPTTGGELVFPDPLSDTGEYSCEARNNGYTPMTSNAVRMEAVERNVGIY 240
Qy 241 AAVLVTLILGLIVFGIMFAYSRGHPDRTKKTSSKKVIYSQPSARSEGEFKOTSSFLV 299
Db 241 AAVLVTLILGLIVFGIMFAYSRGHPDRTKKTSSKKVIYSQPSARSEGEFKOTSSFLV 299

RESULT 13
US-09-909-064-119
; Sequence 119, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanpeter
; APPLICANT: Gettisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, P. Mickey

```

; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909, 064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143, 048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145, 698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146, 222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-909-064-119

Query Match      100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-905-381A-119
; Sequence 119, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905, 381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143, 048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145, 698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146, 222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-905-381A-119

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGTAQYERKLLCFLIALILCSIALGSLVTHSSSEPRIPENNPKLSGASGSPSRV 60
QY 61 EKKFDQDPTTRLVVCYNKKTASVEDRVTFLPTGITFKSVTREDGTTCWVSEEGNSYG 120
DB 61 EKKFDQDPTTRLVVCYNKKTASVEDRVTFLPTGITFKSVTREDGTTCWVSEEGNSYG 120
QY 121 EVKVKLVLPSPKPTVINISSATIGNRAVLTCSQDQSPSEYTFWFDGIVMPTNPKST 180
DB 121 EVKVKLVLPSPKPTVINISSATIGNRAVLTCSQDQSPSEYTFWFDGIVMPTNPKST 180
QY 181 RAFNSSVYLNPTTGGELVFDPLSDTGEYSCEARNGTGTPMTSNAVMEAVERNVGIY 240
DB 181 RAFNSSVYLNPTTGGELVFDPLSDTGEYSCEARNGTGTPMTSNAVMEAVERNVGIY 240
QY 241 AAVLVTLILGLIVFGIMFAYSRGHFDRTKKGTSSKKVIYQPSARSEGFKQTSSFLV 299
DB 241 AAVLVTLILGLIVFGIMFAYSRGHFDRTKKGTSSKKVIYQPSARSEGFKQTSSFLV 299

RESULT 15

US-09-906-618-119
Sequence 119; Application US/09906618
Patent No. 6828146

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Deanoys, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,618

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-618-119

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTAQYERKLLCFLIALILCSIALGSLVTHSSSEPRIPENNPKLSGASGSPSRV 60
DB 1 MGTAQYERKLLCFLIALILCSIALGSLVTHSSSEPRIPENNPKLSGASGSPSRV 60
QY 61 EKKFDQDPTTRLVVCYNKKTASVEDRVTFLPTGITFKSVTREDGTTCWVSEEGNSYG 120
DB 61 EKKFDQDPTTRLVVCYNKKTASVEDRVTFLPTGITFKSVTREDGTTCWVSEEGNSYG 120
QY 121 EVKVKLVLPSPKPTVINISSATIGNRAVLTCSQDQSPSEYTFWFDGIVMPTNPKST 180
DB 121 EVKVKLVLPSPKPTVINISSATIGNRAVLTCSQDQSPSEYTFWFDGIVMPTNPKST 180
QY 181 RAFNSSVYLNPTTGGELVFDPLSDTGEYSCEARNGTGTPMTSNAVMEAVERNVGIY 240
DB 181 RAFNSSVYLNPTTGGELVFDPLSDTGEYSCEARNGTGTPMTSNAVMEAVERNVGIY 240
QY 241 AAVLVTLILGLIVFGIMFAYSRGHFDRTKKGTSSKKVIYQPSARSEGFKQTSSFLV 299
DB 241 AAVLVTLILGLIVFGIMFAYSRGHFDRTKKGTSSKKVIYQPSARSEGFKQTSSFLV 299

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 07:07:56 ; Search time 166 Seconds

(without alignments)

752.596 Million cell updates/sec

Title: US-10-785-433-1

Perfect score: 1544

Sequence: 1 MGTKAQRKLLCLFILAIL.....YSPSARSSEGFKQTSSFLV 299

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1544	100.0	299	3	US-09-799-777-51
4	1544	100.0	299	3	US-09-905-291A-119
5	1544	100.0	299	3	US-09-953-499-1
22	1544	100.0	299	3	US-09-866-050A-189
23	1544	100.0	299	3	US-09-866-050A-331
75	1544	100.0	299	3	US-09-833-245-1300
76	1544	100.0	299	3	US-09-833-245-1301
93	1544	100.0	299	4	US-10-066-269-91
222	1544	100.0	299	4	US-10-223-085-54
226	1544	100.0	299	4	US-10-223-084-54
227	1544	100.0	299	4	US-10-223-088-54
228	1544	100.0	299	4	US-10-223-090-54
229	1544	100.0	299	4	US-10-223-087-54
231	1544	100.0	299	4	US-10-223-083-54
232	1544	100.0	299	4	US-10-223-089-54
362	1544	100.0	299	4	US-10-265-542-1
376	1544	100.0	299	4	US-10-299-976-119
392	1544	100.0	299	4	US-10-299-937-119
395	1544	100.0	299	4	US-10-223-081-54
411	1544	100.0	299	4	US-10-223-082-54
520	1544	100.0	299	4	US-10-298-993-119
522	1544	100.0	299	4	US-10-305-654-54
523	1544	100.0	299	4	US-10-448-923-119
524	1544	100.0	299	4	US-10-291-265-747
525	1544	100.0	299	4	US-10-291-265-747
526	1544	100.0	299	4	US-10-291-265-748
527	1544	100.0	299	4	US-10-449-656-119

528	1544	100.0	299	4	US-10-448-713-119	Sequence 119, App
529	1544	100.0	299	4	US-10-264-237-2666	Sequence 2666, App
532	1544	100.0	299	4	US-10-425-447-119	Sequence 119, App
539	1544	100.0	299	4	US-10-081-056-54	Sequence 54, App
543	1544	100.0	299	4	US-10-601-953-887	Sequence 887, App
544	1544	100.0	299	4	US-10-633-008-1	Sequence 1, App
546	1544	100.0	299	4	US-10-215-371-119	Sequence 119, App
547	1544	100.0	299	4	US-10-785-220-1	Sequence 1, App
548	1544	100.0	299	4	US-10-785-221-1	Sequence 1, App
549	1544	100.0	299	4	US-10-785-433-1	Sequence 119, App
550	1544	100.0	299	4	US-10-797-366-119	Sequence 119, App
551	1544	100.0	299	4	US-10-767-904-1	Sequence 1, App
552	1544	100.0	299	4	US-10-771-187-119	Sequence 119, App
559	1544	100.0	299	5	US-10-767-374-1	Sequence 1, App
560	1544	100.0	299	5	US-10-785-607-1	Sequence 1, App
562	1544	100.0	299	5	US-10-785-351-3	Sequence 3, App
565	1544	100.0	299	5	US-10-931-886-366	Sequence 366, App
567	1544	100.0	299	5	US-10-963-467-119	Sequence 119, App
568	1544	100.0	299	5	US-10-978-255-119	Sequence 119, App
569	1544	100.0	299	5	US-10-955-952-366	Sequence 366, App
570	1544	100.0	299	5	US-10-481-090A-1	Sequence 1, App
571	1544	100.0	299	5	US-10-970-823-119	Sequence 119, App
572	1544	100.0	299	6	US-11-009-868-1	Sequence 1, App
573	1544	100.0	320	5	US-10-128-558-376	Sequence 376, App
574	1544	100.0	336	5	US-10-128-558-193	Sequence 193, App
575	1396.5	90.4	301	3	US-09-764-853-540	Sequence 540, App
576	1396.5	90.4	301	4	US-10-091-438-141	Sequence 141, App
577	1372	88.9	263	3	US-09-953-499-25	Sequence 25, App
578	1372	88.9	263	4	US-10-265-542-25	Sequence 25, App
579	1372	88.9	263	4	US-10-633-008-25	Sequence 25, App
580	1372	88.9	263	4	US-10-785-220-25	Sequence 25, App
581	1372	88.9	263	4	US-10-785-221-25	Sequence 25, App
582	1372	88.9	263	4	US-10-785-433-25	Sequence 25, App
583	1372	88.9	263	4	US-10-767-904-25	Sequence 25, App
584	1372	88.9	263	5	US-10-767-374-25	Sequence 25, App
585	1372	88.9	263	5	US-10-785-607-25	Sequence 25, App
586	1355	87.8	260	3	US-09-953-499-23	Sequence 23, App
587	1355	87.8	260	4	US-10-265-542-23	Sequence 23, App
588	1355	87.8	260	4	US-10-633-008-23	Sequence 23, App
589	1355	87.8	260	4	US-10-785-220-23	Sequence 23, App
590	1355	87.8	260	4	US-10-785-221-23	Sequence 23, App
591	1355	87.8	260	4	US-10-785-433-23	Sequence 23, App
592	1355	87.8	260	4	US-10-767-904-23	Sequence 23, App
593	1355	87.8	260	5	US-10-767-374-23	Sequence 23, App
594	1355	87.8	260	5	US-10-785-607-23	Sequence 23, App
595	1281	79.5	235	4	US-10-291-265-776	Sequence 276, App
596	1228	73.0	225	5	US-10-481-090A-7	Sequence 7, App
597	1114	72.2	208	5	US-10-138-588-10	Sequence 10, App
598	1097	71.0	208	5	US-10-481-090A-8	Sequence 8, App
599	1073.5	69.5	300	3	US-09-953-499-10	Sequence 10, App
600	1073.5	69.5	300	4	US-10-265-542-10	Sequence 10, App
601	1073.5	69.5	300	4	US-10-633-008-10	Sequence 10, App
602	1073.5	69.5	300	4	US-10-785-220-10	Sequence 10, App
603	1073.5	69.5	300	4	US-10-785-221-10	Sequence 10, App
604	1073.5	69.5	300	4	US-10-785-433-10	Sequence 10, App
605	1073.5	69.5	300	4	US-10-767-904-10	Sequence 10, App
606	1073.5	69.5	300	5	US-10-767-374-10	Sequence 10, App
607	1073.5	69.5	300	5	US-10-785-607-10	Sequence 10, App
608	1073.5	69.5	300	5	US-10-785-351-12	Sequence 12, App
609	910	58.9	193	5	US-10-785-351-4	Sequence 4, App
610	763.5	49.4	205	4	US-10-002-631C-176	Sequence 176, App
611	576	37.3	134	3	US-09-866-050A-173	Sequence 173, App
612	525	34.0	141	3	US-09-764-953-536	Sequence 536, App
613	525	34.0	141	3	US-09-764-951-3399	Sequence 3399, App
614	525	34.0	141	4	US-10-091-572-282	Sequence 282, App
615	525	34.0	141	4	US-10-091-438-175	Sequence 175, App
616	431	27.9	298	3	US-09-765-763-38	Sequence 38, App
617	431	27.9	298	3	US-09-799-877-30	Sequence 30, App
618	431	27.9	298	4	US-10-139-849-2	Sequence 2, App
619	431	27.9	298	4	US-10-192-791-2	Sequence 2, App
620	431	27.9	298	4	US-10-601-953-889	Sequence 889, App
621	429	27.8	298	3	US-09-853-161-76	Sequence 76, App
622	429	27.8	298	3	US-09-852-659A-76	Sequence 76, App

623	429	27.8	298	3	US-09-852-797-76	Sequence 76, App1
624	429	27.8	298	4	US-10-058-993-76	Sequence 76, App1
625	429	27.8	298	5	US-10-472-533-461	Sequence 461, App
626	429	27.8	298	5	US-10-951-993-76	Sequence 76, App1
627	428	27.7	298	5	US-10-481-090A-2	Sequence 2, App11
628	427	27.7	310	5	US-10-481-090A-3	Sequence 3, App11
631	424	27.5	310	3	US-09-905-291A-423	Sequence 423, App
700	424	27.5	310	3	US-09-833-245-2045	Sequence 2045, App
701	424	27.5	310	3	US-09-833-245-2046	Sequence 2046, App
702	424	27.5	310	3	US-09-833-245-2047	Sequence 2047, App
709	424	27.5	310	4	US-10-033-244-20	Sequence 20, App1
727	424	27.5	310	4	US-10-050-704-109	Sequence 109, App
728	424	27.5	310	4	US-10-050-704-163	Sequence 163, App
729	424	27.5	310	4	US-10-050-704-164	Sequence 164, App
855	424	27.5	310	4	US-10-223-085-262	Sequence 262, App
858	424	27.5	310	4	US-10-223-084-262	Sequence 262, App
859	424	27.5	310	4	US-10-223-088-262	Sequence 262, App
860	424	27.5	310	4	US-10-223-090-262	Sequence 262, App
861	424	27.5	310	4	US-10-223-087-262	Sequence 262, App
863	424	27.5	310	4	US-10-223-083-262	Sequence 262, App
864	424	27.5	310	4	US-10-223-089-262	Sequence 262, App
993	424	27.5	310	4	US-10-265-542-31	Sequence 31, App1
1007	424	27.5	310	4	US-10-289-976-423	Sequence 423, App
1022	424	27.5	310	4	US-10-299-937-423	Sequence 423, App
1025	424	27.5	310	4	US-10-223-081-262	Sequence 262, App
1041	424	27.5	310	4	US-10-223-082-262	Sequence 262, App
1150	424	27.5	310	4	US-10-298-993-423	Sequence 423, App
1152	424	27.5	310	4	US-10-266-829-65	Sequence 65, App1
1153	424	27.5	310	4	US-10-266-829-90	Sequence 90, App1
1154	424	27.5	310	4	US-10-266-829-91	Sequence 91, App1
1155	424	27.5	310	4	US-10-305-654-262	Sequence 262, App
1156	424	27.5	310	4	US-10-448-923-423	Sequence 423, App
1157	424	27.5	310	4	US-10-439-656-423	Sequence 423, App
1158	424	27.5	310	4	US-10-448-713-423	Sequence 423, App
1159	424	27.5	310	4	US-10-425-447-423	Sequence 423, App
1162	424	27.5	310	4	US-10-081-056-262	Sequence 262, App
1169	424	27.5	310	4	US-10-601-953-888	Sequence 888, App
1173	424	27.5	310	4	US-10-633-008-31	Sequence 31, App1
1174	424	27.5	310	4	US-10-215-371-423	Sequence 423, App
1176	424	27.5	310	4	US-10-797-366-423	Sequence 423, App
1177	424	27.5	310	4	US-10-798-512-109	Sequence 109, App
1178	424	27.5	310	4	US-10-798-512-163	Sequence 163, App
1179	424	27.5	310	4	US-10-798-512-164	Sequence 164, App
1180	424	27.5	310	4	US-10-692-072-20	Sequence 20, App1
1181	424	27.5	310	4	US-10-771-187-423	Sequence 423, App
1182	424	27.5	310	5	US-10-931-886-538	Sequence 538, App
1192	424	27.5	310	5	US-10-963-467-423	Sequence 423, App
1194	424	27.5	310	5	US-10-978-255-423	Sequence 423, App
1195	424	27.5	310	5	US-10-955-952-538	Sequence 538, App
1196	424	27.5	310	5	US-10-878-523-65	Sequence 65, App1
1197	424	27.5	310	5	US-10-878-523-90	Sequence 90, App1
1198	424	27.5	310	5	US-10-878-523-91	Sequence 91, App1
1199	424	27.5	310	5	US-10-970-823-423	Sequence 423, App
1200	424	27.5	310	5	US-10-264-049-3034	Sequence 3034, App
1201	424	27.5	339	4	US-10-266-829-113	Sequence 113, App
1202	424	27.5	339	5	US-10-785-351-9	Sequence 9, App11
1203	424	27.5	76	5	US-10-785-351-11	Sequence 11, App1
1204	412	26.7	76	5	US-09-905-291A-64	Sequence 64, App1
1205	409	26.5	312	3	US-09-953-499-9	Sequence 9, App11
1208	404	26.2	312	3		
1209	404	26.2	312	3		

Search completed: May 16, 2006, 07:13:28
Job time : 190 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 07:12:26 ; Search time 115 Seconds
(without alignments)
122.067 Million cell updates/sec

Title: US-10-785-433-1

Perfect score: 1544

Sequence: 1 MGRKAQVERKLCLFILAIL.....XSQPSARSEGRFKQTSSFLV 299

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA New:*
1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep1.*
2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
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11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
2	1544	100.0	299	9	US-10-973-1158-366
5	1544	100.0	299	11	US-11-000-463-275
6	1544	100.0	299	11	US-11-000-463-747
7	1544	100.0	299	11	US-11-000-463-748
8	1544	100.0	299	11	US-11-173-037-7
9	1544	100.0	299	11	US-11-290-153-366
10	1544	100.0	299	11	US-11-264-096-1300
11	1544	100.0	299	11	US-11-264-096-1301
12	1281	83.0	259	11	US-11-000-463-276
13	1048.5	67.9	300	11	US-11-025-834A-21
14	431	27.9	298	9	US-10-536-366-1
16	424	27.5	310	9	US-10-973-1158-538
20	424	27.5	310	11	US-11-025-834A-15
21	424	27.5	310	11	US-11-280-153-538
22	424	27.5	310	11	US-11-264-096-2045
23	424	27.5	310	11	US-11-264-096-2046
24	424	27.5	310	11	US-11-264-096-2047
25	424	27.5	362	9	US-10-821-234-1148
26	419	27.1	310	9	US-10-536-366-3
27	415	26.9	310	11	US-11-025-834A-13
29	404	26.2	312	9	US-10-973-1158-336

32	404	26.2	312	11	US-11-290-153-336	Sequence 336, App
33	404	26.2	323	9	US-10-536-366-2	Sequence 2, Appl1
34	391	25.3	298	11	US-11-025-834A-14	Sequence 14, Appl
35	390	25.3	212	11	US-11-025-834A-16	Sequence 16, Appl
36	326.5	21.1	265	9	US-10-536-366-5	Sequence 5, Appl1
37	282	18.3	229	9	US-10-536-366-4	Sequence 4, Appl1
43	214.5	13.9	4495	9	US-10-453-372-1002	Sequence 1002, Ap
44	213.5	13.8	1902	9	US-10-453-372-1004	Sequence 1004, Ap
45	213.5	13.8	5636	11	US-11-065-695-20	Sequence 20, Appl
51	207.5	13.4	365	8	US-10-505-928-148	Sequence 148, App
52	207.5	13.4	365	11	US-11-102-978-9	Sequence 9, Appl1
53	207.5	13.4	365	11	US-11-080-991-78	Sequence 78, Appl
55	196	12.7	373	9	US-10-973-1158-388	Sequence 388, App
64	196	12.7	373	11	US-11-290-153-388	Sequence 388, App
65	189	12.2	961	11	US-11-051-724-42	Sequence 42, Appl
66	182	11.8	329	11	US-11-072-512-3709	Sequence 3709, Ap
67	182	11.8	1066	9	US-10-453-372-1090	Sequence 1090, Ap
68	181	11.7	1066	9	US-10-453-372-1084	Sequence 1084, Ap
69	181	11.7	1077	9	US-10-453-372-1086	Sequence 1086, Ap
70	181	11.7	1093	9	US-10-453-372-1088	Sequence 1088, Ap
77	179.5	11.6	316	11	US-11-264-096-2132	Sequence 2152, Ap
79	178.5	11.6	321	11	US-11-159-919-2	Sequence 2, Appl1
80	178.5	11.6	399	11	US-11-159-919-4	Sequence 4, Appl1
81	178.5	11.6	399	11	US-11-264-096-1236	Sequence 1236, Ap
82	178.5	11.6	399	11	US-11-264-096-1237	Sequence 1237, Ap
83	178.5	11.6	847	9	US-10-501-841-61	Sequence 61, Appl
84	177.5	11.5	488	9	US-10-995-561-860	Sequence 860, App
85	177.5	11.5	727	9	US-10-995-561-864	Sequence 864, App
86	177.5	11.5	847	9	US-10-995-561-863	Sequence 863, App
87	177.5	11.5	847	9	US-10-995-561-865	Sequence 865, App
88	176	11.4	390	9	US-10-973-1158-338	Sequence 338, App
92	176	11.4	390	11	US-11-290-153-338	Sequence 338, App
93	176	11.4	707	9	US-10-453-372-598	Sequence 998, App
94	176	11.4	712	9	US-10-453-372-1000	Sequence 1000, Ap
95	174.5	11.3	782	9	US-10-995-561-861	Sequence 861, App
97	174	11.3	398	9	US-10-973-1158-348	Sequence 348, App
100	174	11.3	398	11	US-11-290-153-348	Sequence 348, App
101	173	11.2	1709	9	US-10-995-561-873	Sequence 973, App
102	173	11.2	1709	9	US-10-453-372-410	Sequence 410, App
103	173	11.2	1709	11	US-11-135-855-35	Sequence 35, Appl
104	172	11.1	457	9	US-10-453-372-686	Sequence 686, App
105	172	11.1	457	9	US-10-453-372-690	Sequence 690, App
106	172	11.1	460	9	US-10-453-372-688	Sequence 688, App
107	172	11.1	473	9	US-10-453-372-692	Sequence 692, App
108	172	11.1	473	9	US-10-453-372-694	Sequence 694, App
109	172	11.1	473	9	US-10-453-372-698	Sequence 698, App
110	172	11.1	650	11	US-11-072-512-3395	Sequence 3395, Ap
111	172	11.1	652	9	US-10-453-372-722	Sequence 722, App
112	172	11.1	652	9	US-10-453-372-724	Sequence 724, App
113	172	11.1	670	9	US-10-453-372-670	Sequence 670, App
114	172	11.1	670	9	US-10-453-372-682	Sequence 682, App
115	172	11.1	686	9	US-10-453-372-680	Sequence 680, App
116	172	11.1	961	9	US-10-453-372-726	Sequence 726, App
117	172	11.1	961	9	US-10-453-372-728	Sequence 728, App
118	172	11.1	967	9	US-10-453-372-712	Sequence 712, App
119	172	11.1	967	9	US-10-453-372-714	Sequence 714, App
120	172	11.1	2591	9	US-10-453-372-718	Sequence 718, App
121	172	11.1	2602	9	US-10-453-372-716	Sequence 716, App
122	172	11.1	2617	9	US-10-453-372-666	Sequence 666, App
123	172	11.1	2617	9	US-10-453-372-732	Sequence 732, App
124	172	11.1	2617	9	US-10-453-372-734	Sequence 734, App
125	172	11.1	2617	9	US-10-453-372-736	Sequence 736, App
126	172	11.1	2617	9	US-10-453-372-738	Sequence 738, App
127	172	11.1	2617	9	US-10-453-372-740	Sequence 740, App
128	172	11.1	2617	9	US-10-453-372-742	Sequence 742, App
129	172	11.1	2617	9	US-10-453-372-744	Sequence 744, App
130	172	11.1	2617	9	US-10-453-372-746	Sequence 746, App
131	172	11.1	2617	9	US-10-453-372-748	Sequence 748, App
132	172	11.1	670	9	US-10-453-372-710	Sequence 710, App
133	171	11.1	1119	9	US-10-973-1158-352	Sequence 352, App
134	171	11.1	1119	11	US-11-290-153-352	Sequence 352, App
137	171	11.1	2617	9	US-10-453-372-750	Sequence 750, App
138	171	11.1	396	9	US-10-453-372-750	Sequence 750, App
139	169	10.9	396	9	US-10-453-372-750	Sequence 750, App

140	169	10.9	2828	11	US-11-080-991-54	Sequence 54, App1	230	144.5	9.4	1897	9	US-10-821-234-1635	Sequence 1635, Ap
141	169	10.9	2828	11	US-11-186-284-49	Sequence 49, App1	231	144.5	9.4	1907	11	US-11-000-463-250	Sequence 250, App
142	168.5	10.9	662	9	US-10-493-909-80	Sequence 80, App1	232	144	9.3	319	9	US-10-453-372-300	Sequence 300, App
143	168	10.9	317	11	US-11-072-512-3036	Sequence 3036, Ap	233	144	9.3	765	11	US-11-172-410-19	Sequence 19, App1
144	168	10.9	473	9	US-10-453-372-696	Sequence 696, App	234	143.5	9.3	490	11	US-11-051-720-235	Sequence 325, App
145	167.5	10.8	1571	11	US-11-134-587B-12	Sequence 12, App1	235	143.5	9.3	504	11	US-11-043-806-369	Sequence 369, App
146	167.5	10.8	1700	9	US-10-453-372-416	Sequence 416, App	236	143.5	9.3	504	11	US-11-186-541-3	Sequence 3, App1
147	167.5	10.8	1910	11	US-11-134-587B-2	Sequence 2, App1	237	143.5	9.3	504	11	US-11-051-720-1699	Sequence 1699, Ap
148	167.5	10.8	1910	11	US-11-134-587B-3	Sequence 3, App1	238	143.5	9.3	504	11	US-11-051-720-1700	Sequence 1700, Ap
149	165	10.7	344	11	US-11-080-991-4	Sequence 4, App1	239	143.5	9.3	504	11	US-11-043-806-500	Sequence 500, App
150	165	10.7	344	11	US-11-186-284-20	Sequence 20, App1	240	143.5	9.3	504	11	US-11-043-806-501	Sequence 501, App
151	165	10.7	344	11	US-11-077-386-16	Sequence 16, App1	241	143.5	9.3	584	11	US-11-051-720-324	Sequence 324, App
152	165	10.7	344	11	US-11-097-224B-4	Sequence 4, App1	242	143.5	9.3	584	11	US-11-043-806-368	Sequence 368, App
153	165	10.7	344	11	US-11-050-857-56	Sequence 56, App1	243	143	9.3	315	9	US-10-453-372-290	Sequence 290, App
154	165	10.7	344	11	US-11-050-857-959	Sequence 959, App	244	143	9.3	325	9	US-10-453-372-286	Sequence 286, App
155	165	10.7	344	11	US-11-097-252A-4	Sequence 4, App1	245	143	9.3	344	9	US-10-453-372-284	Sequence 284, App
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157	163	10.6	473	9	US-10-453-372-684	Sequence 684, App	247	142	9.2	325	9	US-10-511-822-11	Sequence 11, App1
158	162.5	10.5	1700	9	US-10-453-372-398	Sequence 398, App	248	142	9.2	325	9	US-10-511-822-12	Sequence 12, App1
159	162.5	10.5	1700	9	US-10-453-372-412	Sequence 412, App	249	141.5	9.2	531	10	US-11-180-885-2	Sequence 2, App1
160	162.5	10.5	1700	9	US-10-453-372-414	Sequence 414, App	250	141.5	9.2	626	10	US-11-180-885-1	Sequence 26, App1
161	162.5	10.5	1700	9	US-10-453-372-418	Sequence 18, App1	251	141.5	9.2	1493	11	US-11-183-116-26	Sequence 298, App
162	161.5	10.5	1571	11	US-11-134-587B-13	Sequence 13, App1	252	141	9.1	307	9	US-10-453-372-298	Sequence 306, App
163	160.5	10.4	543	9	US-10-453-372-756	Sequence 756, App	253	141	9.1	309	9	US-10-453-372-306	Sequence 306, App
164	160.5	10.4	548	9	US-10-453-372-754	Sequence 754, App	254	141	9.1	319	9	US-10-453-372-292	Sequence 292, App
165	160.5	10.4	548	9	US-10-453-372-768	Sequence 768, App	255	141	9.1	320	9	US-10-453-372-296	Sequence 296, App
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170	157.5	10.2	734	11	US-11-093-274-40	Sequence 40, App1	260	141	9.1	336	9	US-10-453-372-314	Sequence 314, App
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181	157	10.2	344	11	US-11-093-274-39	Sequence 39, App1	263	141	9.1	717	11	US-11-051-720-1695	Sequence 1695, Ap
182	156.5	10.1	555	9	US-10-453-372-764	Sequence 764, App	264	141	9.1	860	11	US-11-172-410-2	Sequence 2, App1
183	153	9.9	1338	8	US-10-505-928-634	Sequence 634, App	265	141	9.1	1461	11	US-11-183-116-28	Sequence 28, App1
184	153	9.9	1338	8	US-10-505-928-857	Sequence 857, App	266	140.5	9.1	345	9	US-10-453-372-758	Sequence 758, App
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194	151	9.8	582	11	US-11-051-724-94	Sequence 94, App1	272	138	8.9	517	11	US-11-051-720-1432	Sequence 1432, Ap
195	151	9.8	4419	9	US-10-821-234-1155	Sequence 1155, Ap	273	137.5	8.9	335	9	US-10-948-716-5	Sequence 5, App1
196	151	9.8	324	11	US-11-050-857-57	Sequence 57, App1	274	137	8.9	1189	11	US-11-050-857-953	Sequence 953, App
197	150.5	9.7	1649	9	US-10-995-561-974	Sequence 974, App1	275	137	8.9	1189	11	US-11-051-720-1694	Sequence 1694, Ap
198	150.5	9.7	508	9	US-10-514-534-7	Sequence 7, App1	276	136.5	8.8	337	9	US-10-453-372-760	Sequence 760, App
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202	150	9.7	702	11	US-10-538-066-363	Sequence 363, App	280	136	8.8	555	9	US-10-821-234-1015	Sequence 1015, Ap
203	150	9.7	702	11	US-11-033-039-282	Sequence 282, App	281	135.5	8.8	426	11	US-11-000-463-1394	Sequence 394, App
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206	150	9.7	702	11	US-11-051-720-1451	Sequence 1451, Ap	284	134	8.7	628	11	US-11-080-991-108	Sequence 108, App
207	150	9.7	702	11	US-11-097-252A-2	Sequence 2, App1	285	133.5	8.6	338	9	US-10-996-628-4	Sequence 4, App1
208	150	9.7	719	11	US-11-050-857-551	Sequence 551, App	286	133.5	8.6	426	9	US-10-948-716-1	Sequence 6, App1
209	150	9.7	719	11	US-11-051-720-1381	Sequence 1381, Ap	287	133.5	8.6	428	9	US-10-948-716-3	Sequence 3, App1
210	150	9.7	450	9	US-10-973-1158-378	Sequence 378, App	288	133.5	8.6	666	9	US-10-453-372-368	Sequence 368, App
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212	149	9.7	526	8	US-10-505-928-160	Sequence 32, App1	290	133.5	8.6	1250	11	US-11-137-465-62	Sequence 62, App1
215	149	9.7	647	11	US-11-080-991-32	Sequence 69, App1	291	133.5	8.6	477	9	US-10-973-1158-50	Sequence 50, App1
216	149	9.7	739	9	US-10-493-909-69	Sequence 6, App1	292	133	8.6	477	11	US-11-290-153-50	Sequence 50, App1
217	149	9.7	739	11	US-11-107-028-6	Sequence 67, App1	293	133	8.6	477	11	US-11-139-435-3	Sequence 3, App1
218	149	9.7	3588	11	US-10-995-561-672	Sequence 670, App	294	132	8.5	1007	9	US-10-329-258-23	Sequence 23, App1
219	149	9.7	4346	9	US-10-995-561-671	Sequence 671, App	295	132	8.5	1191	11	US-11-139-435-2	Sequence 2, App1
220	149	9.7	4347	9	US-10-995-561-670	Sequence 670, App	296	132	8.5	892	11	US-11-183-567A-2	Sequence 6, App1
221	149	9.7	4347	9	US-10-995-561-670	Sequence 670, App	297	131.5	8.5	424	9	US-10-948-716-6	Sequence 36, App1
222	149	9.7	4347	9	US-10-995-561-670	Sequence 670, App	298	131.5	8.5	666	9	US-10-453-372-336	Sequence 336, App
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226	146	9.5	394	8	US-10-538-066-754	Sequence 754, App	302	130.5	8.5	757	9	US-10-453-372-350	Sequence 350, App
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228	145	9.4	758	11	US-11-043-693-1	Sequence 1, App1	304	130.5	8.5	757	9	US-10-453-372-350	Sequence 350, App
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322	129.5	8.4	1343	9	US-10-541-814-15	Sequence 15, App1	414	121.5	7.9	255	9	US-10-514-534-8	Sequence 8, App11
323	129	8.4	354	11	US-11-072-512-2965	Sequence 2965, App	415	121.5	7.9	256	11	US-11-054-515-1253	Sequence 1253, App
328	128.5	8.3	419	9	US-10-948-716-4	Sequence 4, App11	416	121.5	7.9	256	11	US-11-266-444-1253	Sequence 1253, App
339	128.5	8.3	696	9	US-10-453-372-334	Sequence 324, App	417	121.5	7.9	258	11	US-11-054-515-1255	Sequence 1255, App
340	128.5	8.3	696	9	US-10-453-372-336	Sequence 346, App	418	121.5	7.9	258	11	US-11-266-444-1255	Sequence 1255, App
341	128.5	8.3	696	9	US-10-453-372-354	Sequence 354, App	419	121.5	7.9	404	11	US-11-197-038-1	Sequence 1, App11
342	128.5	8.3	696	9	US-10-453-372-356	Sequence 356, App	420	121.5	7.9	404	11	US-11-186-422-2	Sequence 2, App11
343	128.5	8.3	696	9	US-10-453-372-358	Sequence 358, App	421	121.5	7.9	404	11	US-11-005-843-1	Sequence 1, App11
344	128.5	8.3	700	9	US-10-453-372-356	Sequence 326, App	422	121.5	7.9	404	11	US-11-197-044-1	Sequence 1, App11
345	128.5	8.3	1343	9	US-10-541-814-2	Sequence 2, App11	423	121	7.8	247	11	US-11-266-444-1429	Sequence 1429, App
346	128	8.3	696	9	US-10-453-372-362	Sequence 362, App	424	121	7.8	249	11	US-11-054-515-1296	Sequence 1296, App
347	127.5	8.3	246	11	US-11-054-515-1630	Sequence 1630, App	425	121	7.8	249	11	US-11-266-444-1296	Sequence 1296, App
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349	127.5	8.3	696	9	US-10-453-372-366	Sequence 366, App	427	121	7.8	242	11	US-11-054-515-1580	Sequence 1580, App
350	127.5	8.3	696	9	US-10-453-372-366	Sequence 366, App	428	120.5	7.8	242	11	US-11-266-444-1580	Sequence 1580, App
351	127.5	8.3	1106	11	US-11-076-427A-16	Sequence 16, App1	429	120.5	7.8	242	11	US-11-266-444-1580	Sequence 1580, App
352	127.5	8.3	1106	11	US-11-075-047A-119	Sequence 119, App	430	120.5	7.8	256	11	US-11-050-857-58	Sequence 58, App1
353	127	8.2	248	11	US-11-054-515-1963	Sequence 1963, App	431	120.5	7.8	277	9	US-10-996-007B-16	Sequence 16, App1
354	127	8.2	248	11	US-11-266-444-1963	Sequence 1963, App	432	120.5	7.8	757	11	US-11-264-096-1856	Sequence 1856, App
355	127	8.2	515	11	US-11-083-274-38	Sequence 38, App1	433	120.5	7.8	757	9	US-10-453-372-352	Sequence 352, App
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357	126.5	8.2	250	11	US-11-266-444-1529	Sequence 1529, App	435	120.5	7.8	778	9	US-10-453-372-350	Sequence 350, App1
358	126.5	8.2	1433	11	US-11-094-519A-40	Sequence 40, App1	436	120	7.8	23	11	US-11-173-037-1	Sequence 1, App11
360	126	8.2	708	9	US-10-511-538-229	Sequence 229, App1	437	120	7.8	245	11	US-11-054-515-1757	Sequence 1757, App
365	126	8.2	764	11	US-11-104-110-8	Sequence 8, App11	438	120	7.8	245	11	US-11-266-444-1757	Sequence 1757, App
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376	124.5	8.1	917	9	US-10-493-909-76	Sequence 76, App1	449	119	7.7	686	11	US-11-051-724-48	Sequence 48, App1
377	124.5	8.1	917	9	US-10-493-909-87	Sequence 87, App1	450	119	7.7	686	11	US-11-051-724-50	Sequence 50, App1
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379	124	8.0	249	11	US-11-266-444-1272	Sequence 1272, App	452	118.5	7.7	192	9	US-10-514-534-9	Sequence 9, App11
380	124	8.0	253	11	US-11-054-515-1199	Sequence 1199, App	453	118.5	7.7	246	11	US-11-054-515-1996	Sequence 1996, App
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383	124	8.0	686	11	US-11-051-724-52	Sequence 52, App1	456	118.5	7.7	248	11	US-11-266-444-1040	Sequence 1040, App
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388	123.5	8.0	466	9	US-10-979-095-1	Sequence 1, App11	462	118	7.6	245	11	US-11-054-515-1477	Sequence 1477, App
389	123.5	8.0	696	9	US-10-453-372-360	Sequence 360, App	463	118	7.6	245	11	US-11-266-444-1477	Sequence 1477, App
390	123.5	8.0	885	11	US-11-072-512-2946	Sequence 2946, App	464	118	7.6	422	9	US-10-917-905-3	Sequence 3, App11
391	123.5	8.0	915	11	US-11-144-987-22	Sequence 22, App1	465	118	7.6	806	10	US-11-251-865-22	Sequence 20, App1
392	123.5	8.0	915	11	US-11-205-935-22	Sequence 22, App1	466	118	7.6	924	9	US-10-857-780-20	Sequence 20, App1
393	123.5	8.0	917	11	US-11-144-987-24	Sequence 24, App1	467	118	7.6	924	9	US-10-493-909-67	Sequence 67, App1
394	123.5	8.0	917	11	US-11-144-987-26	Sequence 26, App1	468	118	7.6	924	11	US-11-107-028-26	Sequence 26, App1
395	123.5	8.0	917	11	US-11-205-935-24	Sequence 24, App1	469	117.5	7.6	244	11	US-11-054-515-1639	Sequence 1639, App
396	123.5	8.0	917	11	US-11-205-935-26	Sequence 26, App1	470	117.5	7.6	244	11	US-11-266-444-1639	Sequence 1639, App
397	123	8.0	248	11	US-11-054-515-2070	Sequence 2070, App	471	117.5	7.6	247	11	US-11-054-515-1527	Sequence 1527, App
398	123	8.0	335	9	US-10-948-716-2	Sequence 2, App11	472	117.5	7.6	247	11	US-11-266-444-1527	Sequence 1527, App
399	122.5	7.9	424	9	US-10-948-716-10	Sequence 10, App1	473	117.5	7.6	328	9	US-10-996-007B-14	Sequence 14, App1
400	122.5	7.9	915	11	US-11-144-987-16	Sequence 16, App1	474	117.5	7.6	328	9	US-10-501-035-33	Sequence 33, App
401	122.5	7.9	915	11	US-11-205-935-16	Sequence 16, App1	475	117.5	7.6	1084	9	US-10-517-905-12	Sequence 12, App1
402	122.5	7.9	917	11	US-11-144-987-18	Sequence 18, App1	476	117.5	7.6	1084	9	US-10-517-905-63	Sequence 23, App1
403	122.5	7.9	917	11	US-11-144-987-20	Sequence 20, App1	477	117.5	7.6	1085	9	US-10-517-905-63	Sequence 23, App1
404	122.5	7.9	917	11	US-11-205-935-18	Sequence 18, App1	478	117.5	7.6	1086	9	US-10-517-905-8	Sequence 8, App11
405	122.5	7.9	917	11	US-11-205-935-20	Sequence 20, App1	479	117.5	7.6	1089	9	US-10-517-905-2	Sequence 2, App11
406	122.5	7.9	1150	11	US-11-139-435-1	Sequence 1, App11	480	117.5	7.6	1089	9	US-10-517-905-4	Sequence 4, App11
407	122.5	7.9	249	11	US-11-054-515-1347	Sequence 1347, App	481	117.5	7.6	1089	9	US-10-517-905-4	Sequence 4, App11
408	122	7.9	249	11	US-11-054-515-1347	Sequence 1347, App	488	117.5	7.6	1089	9	US-10-517-905-21	Sequence 21, App1

489	117.5	7.6	1089	9	US-10-517-905-25	Sequence 25, Appl	562	114.5	7.4	244	11	US-11-054-515-1214	Sequence 1214, Ap
490	117.5	7.6	1089	9	US-10-517-905-27	Sequence 27, Appl	563	114.5	7.4	244	11	US-11-266-444-1210	Sequence 1210, Ap
491	117.5	7.6	1089	11	US-11-148-770-32	Sequence 12, Appl	564	114.5	7.4	244	11	US-11-266-444-1214	Sequence 1214, Ap
492	117.5	7.6	1089	11	US-11-076-427A-14	Sequence 14, Appl	565	114.5	7.4	252	11	US-11-054-515-1139	Sequence 1129, Ap
493	117.5	7.6	1089	11	US-11-075-047A-117	Sequence 117, Appl	566	114.5	7.4	252	11	US-11-266-444-1119	Sequence 1129, Ap
494	117.5	7.6	1089	11	US-11-177-894-26	Sequence 26, Appl	567	114.5	7.4	266	9	US-10-995-561-44	Sequence 544, App
495	117.5	7.6	1089	11	US-11-177-894-27	Sequence 27, Appl	568	114.5	7.4	269	9	US-10-839-799-109	Sequence 109, App
496	117.5	7.6	1089	11	US-11-177-894-28	Sequence 28, Appl	569	114.5	7.4	352	11	US-11-051-720-1335	Sequence 1325, Ap
497	117.5	7.6	1089	11	US-11-177-894-29	Sequence 29, Appl	570	114.5	7.4	354	11	US-11-051-720-1324	Sequence 1324, Ap
498	117.5	7.6	1089	11	US-11-233-510-28	Sequence 28, Appl	571	114.5	7.4	409	9	US-10-821-234-692	Sequence 892, App
499	117.5	7.6	1090	9	US-10-517-905-10	Sequence 10, Appl	572	114.5	7.4	439	11	US-11-198-819-12	Sequence 12, Appl
500	117.5	7.6	1451	9	US-10-995-561-829	Sequence 829, App	573	114.5	7.4	439	11	US-11-299-182-8	Sequence 8, Appl1
501	117	7.6	249	11	US-11-054-515-1753	Sequence 1753, Ap	574	114.5	7.4	464	10	US-11-219-563-132	Sequence 132, App
502	117	7.6	249	11	US-11-266-444-1753	Sequence 1240, Ap	575	114.5	7.4	464	11	US-11-218-813-132	Sequence 132, App
503	117	7.6	257	11	US-11-054-515-1240	Sequence 1240, Ap	576	114.5	7.4	247	11	US-11-054-515-1455	Sequence 1455, Ap
504	117	7.6	257	11	US-11-266-444-1240	Sequence 1240, Ap	577	114	7.4	247	11	US-11-266-444-1455	Sequence 1455, Ap
505	117	7.6	276	11	US-11-038-901-19	Sequence 19, Appl	578	114	7.4	248	11	US-11-054-515-1976	Sequence 1976, Ap
506	117	7.6	305	11	US-11-087-177-11	Sequence 11, Appl	579	114	7.4	248	11	US-11-266-444-1976	Sequence 1976, Ap
507	117	7.6	305	11	US-11-087-177-13	Sequence 13, Appl	580	114	7.4	251	11	US-11-054-515-1536	Sequence 1536, Ap
508	117	7.6	391	9	US-10-996-628-2	Sequence 2, Appl1	581	114	7.4	251	11	US-11-266-444-1536	Sequence 1536, Ap
509	116.5	7.5	250	11	US-11-054-515-1203	Sequence 1203, Ap	582	114	7.4	305	9	US-10-055-877-126	Sequence 126, App
510	116.5	7.5	250	11	US-11-054-515-1212	Sequence 1212, Ap	583	114	7.4	305	9	US-10-055-877-264	Sequence 264, App
511	116.5	7.5	250	11	US-11-266-444-1203	Sequence 1203, Ap	584	114	7.4	305	11	US-11-080-091-2	Sequence 2, Appl1
512	116.5	7.5	250	11	US-11-266-444-1212	Sequence 1212, Ap	585	114	7.4	305	11	US-11-087-177-7	Sequence 7, Appl1
513	116.5	7.5	252	11	US-11-054-515-898	Sequence 898, App	586	114	7.4	346	11	US-11-050-857-553	Sequence 553, App
514	116.5	7.5	252	11	US-11-266-444-898	Sequence 898, App	587	114	7.4	346	11	US-11-051-720-1383	Sequence 1383, Ap
515	116.5	7.5	259	9	US-10-995-561-883	Sequence 883, App	588	114	7.4	461	11	US-11-197-038-32	Sequence 32, Appl
516	116.5	7.5	349	11	US-11-235-776A-13	Sequence 13, Appl	589	114	7.4	461	11	US-11-197-644-32	Sequence 32, Appl
517	116.5	7.5	426	9	US-10-948-716-9	Sequence 9, Appl1	590	113.5	7.4	249	11	US-11-054-515-1168	Sequence 1168, Ap
518	116.5	7.5	458	11	US-11-235-776A-11	Sequence 11, Appl	591	113.5	7.4	249	11	US-11-266-444-1168	Sequence 1168, Ap
519	116.5	7.5	543	9	US-10-495-664-3	Sequence 3, Appl1	592	113.5	7.4	251	11	US-11-054-515-1546	Sequence 1546, Ap
520	116.5	7.5	602	9	US-10-493-909-51	Sequence 51, Appl1	593	113.5	7.4	251	11	US-11-266-444-1546	Sequence 1546, Ap
521	116.5	7.5	648	9	US-10-917-905-6	Sequence 6, Appl1	594	113.5	7.4	258	11	US-11-054-515-1243	Sequence 1243, Ap
522	116	7.5	263	11	US-11-054-515-1278	Sequence 1278, Ap	595	113.5	7.4	269	11	US-11-266-444-1243	Sequence 1243, Ap
523	116	7.5	263	11	US-11-266-444-1278	Sequence 1278, Ap	596	113.5	7.4	269	11	US-11-266-444-1243	Sequence 1243, Ap
524	116	7.5	305	11	US-11-080-091-13	Sequence 13, Appl	597	113.5	7.4	288	9	US-10-821-234-1062	Sequence 1062, App
525	116	7.5	341	9	US-10-514-534-6	Sequence 6, Appl1	598	113.5	7.4	297	9	US-10-453-372-766	Sequence 766, App
526	115.5	7.5	238	11	US-11-052-554A-51	Sequence 51, Appl	599	113	7.3	22	11	US-11-173-037-2	Sequence 2, Appl1
527	115.5	7.5	238	11	US-11-052-554A-52	Sequence 52, Appl	600	113	7.3	194	9	US-11-233-798-10	Sequence 10, Appl
528	115.5	7.5	240	11	US-11-000-63-248	Sequence 248, App	601	113	7.3	447	9	US-10-884-730-379	Sequence 379, App
529	115.5	7.5	248	11	US-11-054-515-1387	Sequence 1387, Ap	602	113	7.3	448	11	US-11-299-182-14	Sequence 18, Appl
530	115.5	7.5	248	11	US-11-266-444-1387	Sequence 1387, Ap	603	113	7.3	489	11	US-11-299-182-14	Sequence 18, Appl
531	115.5	7.5	250	11	US-11-054-515-1370	Sequence 1370, Ap	604	113	7.3	652	11	US-11-299-182-4	Sequence 4, Appl1
532	115.5	7.5	250	11	US-11-266-444-1370	Sequence 1370, Ap	605	112.5	7.3	248	11	US-11-054-515-2086	Sequence 2086, Ap
533	115.5	7.5	277	9	US-10-996-007B-13	Sequence 13, Appl	606	112.5	7.3	248	11	US-11-266-444-2086	Sequence 2086, Ap
534	115.5	7.5	374	11	US-11-000-663-453	Sequence 453, App	607	112.5	7.3	250	11	US-11-054-515-1348	Sequence 1348, Ap
535	115.5	7.5	381	11	US-11-197-038-3	Sequence 3, Appl1	608	112.5	7.3	250	11	US-11-266-444-1348	Sequence 1348, Ap
536	115.5	7.5	381	11	US-11-197-038-2	Sequence 2, Appl1	609	112.5	7.3	421	11	US-11-051-724-96	Sequence 96, Appl
537	115.5	7.5	382	11	US-11-197-038-4	Sequence 4, Appl1	610	112.5	7.3	421	11	US-11-051-724-96	Sequence 96, Appl
538	115.5	7.5	382	11	US-11-197-644-2	Sequence 2, Appl1	617	112.5	7.3	463	11	US-11-102-240-86	Sequence 86, Appl
539	115.5	7.5	426	9	US-10-821-234-1585	Sequence 1585, Ap	618	112.5	7.3	463	11	US-11-103-195-86	Sequence 86, Appl
540	115.5	7.5	595	11	US-11-264-096-2258	Sequence 2258, Ap	619	112.5	7.3	619	11	US-11-072-512-2048	Sequence 2048, App
541	115	7.4	241	11	US-11-054-515-1788	Sequence 1788, Ap	620	112	7.3	22	11	US-11-173-037-3	Sequence 3, Appl1
542	115	7.4	283	9	US-10-453-372-850	Sequence 850, App	621	112	7.3	245	11	US-11-054-515-1422	Sequence 1422, Ap
543	115	7.4	283	9	US-10-453-372-836	Sequence 836, App	622	112	7.3	245	11	US-11-054-515-1460	Sequence 1460, Ap
544	115	7.4	290	9	US-10-453-372-842	Sequence 842, App	623	112	7.3	245	11	US-11-054-515-1754	Sequence 1754, Ap
545	115	7.4	290	9	US-10-453-372-848	Sequence 848, App	624	112	7.3	245	11	US-11-054-515-1754	Sequence 1754, Ap
546	115	7.4	290	9	US-10-453-372-848	Sequence 848, App	625	112	7.3	245	11	US-11-054-515-1754	Sequence 1754, Ap
547	115	7.4	290	9	US-10-453-372-848	Sequence 848, App	626	112	7.3	245	11	US-11-054-515-1754	Sequence 1754, Ap
548	115	7.4	290	11	US-11-113-424-77	Sequence 77, Appl1	627	112	7.3	245	11	US-11-266-444-1464	Sequence 1464, Ap
549	115	7.4	290	11	US-11-245-713-1	Sequence 1, Appl1	628	112	7.3	245	11	US-11-266-444-1464	Sequence 1464, Ap
550	115	7.4	290	11	US-11-264-096-763	Sequence 763, App	629	112	7.3	245	11	US-11-266-444-1754	Sequence 1754, Ap
551	115	7.4	295	9	US-10-453-372-840	Sequence 840, App	630	112	7.3	245	11	US-11-266-444-1754	Sequence 1754, Ap
552	115	7.4	308	11	US-11-235-776A-1	Sequence 1, Appl1	631	112	7.3	246	11	US-11-054-515-1847	Sequence 1847, Ap
553	115	7.4	339	11	US-11-197-038-4	Sequence 4, Appl1	632	112	7.3	246	11	US-11-266-444-1847	Sequence 1847, Ap
554	115	7.4	339	11	US-11-005-843-2	Sequence 2, Appl1	633	112	7.3	247	11	US-11-054-515-878	Sequence 878, App
555	115	7.4	346	11	US-11-197-644-4	Sequence 4, Appl1	634	112	7.3	247	11	US-11-266-444-878	Sequence 878, App
556	115	7.4	346	11	US-11-197-644-35	Sequence 35, Appl1	635	112	7.3	248	11	US-11-054-515-2000	Sequence 2000, Ap
557	115	7.4	346	11	US-11-197-644-35	Sequence 35, Appl1	636	112	7.3	248	11	US-11-266-444-2000	Sequence 2000, Ap
558	115	7.4	346	11	US-11-235-776A-3	Sequence 3, Appl1	637	112	7.3	259	11	US-11-054-515-1497	Sequence 1497, Ap
559	115	7.4	551	11	US-11-235-776A-7	Sequence 7, Appl1	638	112	7.3	259	11	US-11-266-444-1497	Sequence 1497, Ap
560	115	7.4	551	11	US-11-235-776A-9	Sequence 9, Appl1	639	112	7.3	267	9	US-10-995-561-543	Sequence 543, App
561	114.5	7.4	244	11	US-11-054-515-1210	Sequence 1210, Ap	640	112	7.3	363	11	US-11-051-720-1326	Sequence 1326, Ap

641	112	7.3	421	11	US-11-051-724-100	Sequence 100, App	714	109.5	7.1	252	11	US-11-054-515-897	Sequence 897, App
642	112	7.3	766	11	US-11-147-047-27	Sequence 27, Appl	715	109.5	7.1	252	11	US-11-054-515-1016	Sequence 1016, Ap
643	111.5	7.2	229	9	US-10-496-284-11	Sequence 11, Appl	716	109.5	7.1	252	11	US-11-054-515-1135	Sequence 1135, Ap
644	111.5	7.2	228	11	US-11-054-515-1438	Sequence 1438, Ap	717	109.5	7.1	252	11	US-11-266-444-897	Sequence 897, App
645	111.5	7.2	242	11	US-11-266-444-1438	Sequence 1438, Ap	718	109.5	7.1	252	11	US-11-266-444-1016	Sequence 1016, Ap
646	111.5	7.2	244	11	US-11-054-515-1507	Sequence 1507, Ap	719	109.5	7.1	252	11	US-11-266-444-1135	Sequence 1135, Ap
647	111.5	7.2	244	11	US-11-054-515-1842	Sequence 1842, Ap	720	109.5	7.1	260	11	US-11-054-515-1250	Sequence 1250, Ap
648	111.5	7.2	244	11	US-11-054-515-1842	Sequence 2058, Ap	721	109.5	7.1	260	11	US-11-266-444-1250	Sequence 1250, Ap
649	111.5	7.2	244	11	US-11-266-444-1507	Sequence 1507, Ap	722	109.5	7.1	224	9	US-10-055-877-128	Sequence 128, App
650	111.5	7.2	244	11	US-11-266-444-1842	Sequence 1842, Ap	723	109.5	7.1	307	9	US-10-055-877-263	Sequence 263, App
651	111.5	7.2	244	11	US-11-266-444-2058	Sequence 2058, Ap	724	109.5	7.1	372	10	US-11-251-465-71	Sequence 71, Appl
652	111.5	7.2	252	11	US-11-054-515-1131	Sequence 1131, Ap	725	109.5	7.1	500	11	US-11-072-512-2825	Sequence 2825, Ap
653	111.5	7.2	252	11	US-11-266-444-1131	Sequence 1131, Ap	726	109.5	7.1	728	8	US-10-511-937-2418	Sequence 2418, Ap
654	111.5	7.2	261	11	US-11-054-515-1503	Sequence 1503, Ap	727	109.5	7.1	738	9	US-10-995-561-692	Sequence 692, App
655	111.5	7.2	261	11	US-11-266-444-1503	Sequence 1503, Ap	728	109.5	7.1	738	9	US-10-995-561-693	Sequence 693, App
656	111.5	7.2	322	9	US-10-979-095-8	Sequence 8, Appl	729	109	7.1	240	11	US-11-054-515-1905	Sequence 1905, Ap
657	111.5	7.2	567	11	US-11-000-463-400	Sequence 400, App	730	109	7.1	240	11	US-11-054-515-2030	Sequence 2030, Ap
658	111.5	7.2	592	9	US-10-016-686-4	Sequence 4, Appl	731	109	7.1	240	11	US-11-054-515-2113	Sequence 2113, Ap
659	111	7.2	247	11	US-11-054-515-1099	Sequence 1099, Ap	732	109	7.1	240	11	US-11-266-444-1905	Sequence 1905, Ap
660	111	7.2	247	11	US-11-266-444-1099	Sequence 1099, Ap	733	109	7.1	240	11	US-11-266-444-2030	Sequence 2030, Ap
661	111	7.2	249	11	US-11-054-515-1891	Sequence 1891, Ap	734	109	7.1	240	11	US-11-266-444-2113	Sequence 2113, Ap
662	111	7.2	249	11	US-11-266-444-1891	Sequence 1891, Ap	735	109	7.1	245	11	US-11-054-515-1528	Sequence 1528, Ap
663	111	7.2	251	11	US-11-054-515-1122	Sequence 1122, Ap	736	109	7.1	245	11	US-11-266-444-1528	Sequence 1528, Ap
664	111	7.2	251	11	US-11-054-515-1122	Sequence 1223, Ap	737	109	7.1	248	9	US-10-923-327-16	Sequence 16, Appl
665	111	7.2	251	11	US-11-054-515-1805	Sequence 1805, Ap	738	109	7.1	249	11	US-11-054-515-1894	Sequence 1894, Ap
666	111	7.2	251	11	US-11-054-515-1812	Sequence 1812, Ap	739	109	7.1	249	11	US-11-054-515-2122	Sequence 2122, Ap
667	111	7.2	251	11	US-11-266-444-1122	Sequence 1122, Ap	740	109	7.1	249	11	US-11-266-444-1894	Sequence 1894, Ap
668	111	7.2	251	11	US-11-266-444-1122	Sequence 1223, Ap	741	109	7.1	249	11	US-11-266-444-2122	Sequence 2122, Ap
669	111	7.2	251	11	US-11-266-444-1805	Sequence 1805, Ap	742	109	7.1	251	11	US-11-054-515-1487	Sequence 1487, Ap
670	111	7.2	251	11	US-11-266-444-1812	Sequence 1812, Ap	743	109	7.1	251	11	US-11-266-444-1487	Sequence 1487, Ap
671	111	7.2	254	11	US-11-054-515-1966	Sequence 1966, Ap	744	109	7.1	259	11	US-11-054-515-1375	Sequence 1375, Ap
672	111	7.2	254	11	US-11-266-444-11966	Sequence 1966, Ap	745	109	7.1	259	11	US-11-054-515-1481	Sequence 1481, Ap
673	111	7.2	255	11	US-11-054-515-863	Sequence 863, App	746	109	7.1	259	11	US-11-266-444-1275	Sequence 1275, Ap
674	111	7.2	255	11	US-11-266-444-863	Sequence 863, App	747	109	7.1	259	11	US-11-266-444-1481	Sequence 1481, Ap
675	111	7.2	257	11	US-11-054-515-1553	Sequence 1553, App	748	109	7.1	269	9	US-10-821-334-1308	Sequence 1308, Ap
676	111	7.2	257	11	US-11-266-444-1553	Sequence 1553, Ap	749	109	7.1	302	9	US-10-453-372-788	Sequence 788, App
677	111	7.2	327	11	US-11-233-798-2	Sequence 2, Appl	750	109	7.1	302	9	US-10-453-372-792	Sequence 792, App
678	111	7.2	336	11	US-11-113-424-83	Sequence 83, Appl	751	109	7.1	316	11	US-11-197-038-6	Sequence 6, Appl
679	110.5	7.2	244	11	US-11-054-515-1491	Sequence 1491, Ap	752	109	7.1	316	11	US-11-197-644-6	Sequence 6, Appl
680	110.5	7.2	244	11	US-11-266-444-1491	Sequence 1491, Ap	753	109	7.1	317	11	US-11-197-038-5	Sequence 5, Appl
681	110.5	7.2	246	11	US-11-054-515-1369	Sequence 1369, Ap	754	109	7.1	317	11	US-11-197-644-5	Sequence 5, Appl
682	110.5	7.2	246	11	US-11-266-444-1369	Sequence 1369, Ap	755	109	7.1	333	11	US-11-197-038-37	Sequence 37, Appl
683	110.5	7.2	248	11	US-11-054-515-1273	Sequence 1273, Ap	756	109	7.1	323	11	US-11-197-644-37	Sequence 37, Appl
684	110.5	7.2	248	11	US-11-054-515-1331	Sequence 1331, Ap	757	109	7.1	324	11	US-11-197-644-36	Sequence 36, Appl
685	110.5	7.2	248	11	US-11-054-515-1363	Sequence 1363, Ap	758	109	7.1	334	11	US-11-197-644-36	Sequence 36, Appl
686	110.5	7.2	248	11	US-11-266-444-1273	Sequence 1273, Ap	759	109	7.1	402	9	US-10-204-639-43	Sequence 43, Appl
687	110.5	7.2	248	11	US-11-266-444-1331	Sequence 1331, Ap	760	109	7.1	412	9	US-11-174-150-47	Sequence 47, Appl
688	110.5	7.2	248	11	US-11-266-444-1363	Sequence 1363, Ap	761	109	7.1	516	11	US-11-185-438-20	Sequence 20, Appl
689	110.5	7.2	250	11	US-11-054-515-834	Sequence 834, App	762	109	7.1	516	11	US-11-185-438-20	Sequence 20, Appl
690	110.5	7.2	250	11	US-11-054-515-1367	Sequence 1367, App	763	109	7.1	516	11	US-11-185-438-20	Sequence 20, Appl
691	110.5	7.2	250	11	US-11-266-444-834	Sequence 834, App	764	109	7.1	516	11	US-11-185-438-20	Sequence 20, Appl
692	110.5	7.2	250	11	US-11-266-444-1367	Sequence 1367, App	765	109	7.1	516	11	US-11-185-438-20	Sequence 20, Appl
693	110.5	7.2	254	11	US-11-054-515-1865	Sequence 1865, Ap	766	109	7.1	628	11	US-11-147-047-45	Sequence 45, Appl
694	110.5	7.2	254	11	US-11-266-444-1865	Sequence 1865, Ap	767	109	7.1	628	11	US-11-147-047-45	Sequence 45, Appl
695	110.5	7.2	256	11	US-11-054-515-1600	Sequence 1600, Ap	768	109	7.1	640	9	US-10-917-905-1	Sequence 1, Appl
696	110.5	7.2	256	11	US-11-266-444-1600	Sequence 1600, Ap	769	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appl
697	110.5	7.2	258	11	US-11-054-515-1265	Sequence 1265, Ap	770	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appl
698	110.5	7.2	258	11	US-11-054-515-1265	Sequence 1265, Ap	771	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appl
699	110.5	7.2	258	11	US-11-266-444-1265	Sequence 1265, Ap	772	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appl
700	110.5	7.2	258	11	US-11-266-444-1265	Sequence 1265, Ap	773	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appl
701	110.5	7.2	258	11	US-11-266-444-1265	Sequence 1265, Ap	774	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appl
702	110	7.1	245	11	US-11-233-798-6	Sequence 6, Appl	775	108.5	7.0	244	11	US-11-266-444-1692	Sequence 1692, Ap
703	110	7.1	245	11	US-11-054-515-1457	Sequence 1457, Ap	776	108.5	7.0	244	11	US-11-266-444-1692	Sequence 1692, Ap
704	110	7.1	245	11	US-11-266-444-1457	Sequence 1457, Ap	777	108.5	7.0	248	11	US-11-054-515-1031	Sequence 1031, Ap
705	110	7.1	249	11	US-11-054-515-2120	Sequence 2120, Ap	778	108.5	7.0	248	11	US-11-266-444-1031	Sequence 1031, Ap
706	110	7.1	249	11	US-11-266-444-2120	Sequence 2120, Ap	779	108.5	7.0	251	11	US-11-054-515-1121	Sequence 1121, Ap
707	110	7.1	302	9	US-10-453-372-780	Sequence 780, App	780	108.5	7.0	251	11	US-11-054-515-1373	Sequence 1373, Ap
708	110	7.1	302	9	US-10-453-372-782	Sequence 782, App	781	108.5	7.0	251	11	US-11-266-444-1121	Sequence 1121, Ap
709	110	7.1	346	11	US-11-233-7764-5	Sequence 5, Appl	782	108.5	7.0	251	11	US-11-266-444-1121	Sequence 1121, Ap
710	109.5	7.1	433	9	US-10-453-372-770	Sequence 770, App	783	108.5	7.0	251	11	US-11-266-444-1121	Sequence 1121, Ap
711	109.5	7.1	248	11	US-11-054-515-1254	Sequence 1254, Ap	784	108.5	7.0	252	11	US-11-054-515-1163	Sequence 1163, Ap
712	109.5	7.1	248	11	US-11-266-444-1254	Sequence 1254, Ap	785	108.5	7.0	252	11	US-11-266-444-1163	Sequence 1163, Ap
713	109.5	7.1	250	11	US-11-054-515-7	Sequence 7, Appl	786	108.5	7.0	256	11	US-11-054-515-1279	Sequence 1279, Ap
			250	11	US-11-266-444-7	Sequence 7, Appl	787	108.5	7.0	256	11	US-11-266-444-1279	Sequence 1279, Ap

804	108.5	7.0	258	11	US-11-054-515-1274	Sequence 1274, Ap	888	107.5	7.0	250	11	US-11-266-444-1280	Sequence 1280, Ap
805	108.5	7.0	258	11	US-11-266-444-1239	Sequence 1239, Ap	889	107.5	7.0	250	11	US-11-266-444-1414	Sequence 1414, Ap
806	108.5	7.0	258	11	US-11-266-444-1274	Sequence 1274, Ap	890	107.5	7.0	252	11	US-11-054-515-1500	Sequence 1500, Ap
808	108.5	7.0	334	9	US-10-973-1158-520	Sequence 520, App	891	107.5	7.0	252	11	US-11-054-515-1954	Sequence 1954, Ap
816	108.5	7.0	334	11	US-11-290-153-520	Sequence 520, App	892	107.5	7.0	252	11	US-11-266-444-1500	Sequence 1500, Ap
817	108.5	7.0	934	11	US-11-046-653-4	Sequence 4, Appl1	893	107.5	7.0	252	11	US-11-266-444-1954	Sequence 1954, Ap
819	108.5	7.0	934	11	US-10-973-1158-146	Sequence 146, App	894	107.5	7.0	282	9	US-10-055-877-127	Sequence 127, App
822	108.5	7.0	945	9	US-11-183-136-18	Sequence 18, Appl	895	107.5	7.0	282	11	US-11-087-177-9	Sequence 9, Appl1
823	108.5	7.0	945	11	US-11-183-136-20	Sequence 20, Appl	896	107.5	7.0	462	11	US-11-177-648-26	Sequence 26, Appl
824	108.5	7.0	945	11	US-11-183-136-20	Sequence 20, Appl	897	107.5	7.0	462	11	US-11-177-648-78	Sequence 78, Appl
825	108.5	7.0	945	11	US-11-290-153-146	Sequence 146, App	898	107.5	7.0	462	11	US-11-177-648-98	Sequence 98, Appl
826	108.5	7.0	203	11	US-11-197-038-18	Sequence 18, Appl	899	107.5	7.0	479	11	US-11-147-047-44	Sequence 44, Appl1
827	108.5	7.0	203	11	US-11-197-644-18	Sequence 18, Appl	901	107.5	7.0	653	9	US-10-917-905-2	Sequence 2, Appl1
828	108.5	7.0	204	11	US-11-197-038-17	Sequence 17, Appl	902	107.5	7.0	653	9	US-10-917-905-2	Sequence 2, Appl1
829	108.5	7.0	204	11	US-11-197-644-17	Sequence 17, Appl	905	107.5	7.0	653	9	US-10-917-905-2	Sequence 2, Appl1
830	108.5	7.0	228	11	US-11-197-038-20	Sequence 20, Appl	906	107.5	7.0	653	11	US-11-135-855-25	Sequence 25, Appl
831	108.5	7.0	228	11	US-11-197-644-20	Sequence 20, Appl	907	107.5	7.0	653	11	US-11-290-153-438	Sequence 438, App
832	108.5	7.0	229	11	US-11-197-038-19	Sequence 19, Appl	908	107.5	6.9	213	9	US-10-948-718-11	Sequence 11, Appl
833	108.5	7.0	229	11	US-11-197-644-19	Sequence 19, Appl	909	107.5	6.9	237	11	US-11-204-709-23	Sequence 23, Appl
834	108.5	7.0	235	11	US-11-197-644-18	Sequence 18, Appl	910	107.5	6.9	240	11	US-11-089-803-23	Sequence 23, Appl
835	108.5	7.0	240	11	US-11-204-709-18	Sequence 18, Appl	911	107.5	6.9	240	11	US-11-218-234-23	Sequence 23, Appl
836	108.5	7.0	240	11	US-11-054-515-2007	Sequence 2007, Ap	912	107.5	6.9	240	11	US-11-218-234-23	Sequence 23, Appl
837	108.5	7.0	240	11	US-11-054-515-2016	Sequence 2016, Ap	913	107.5	6.9	240	11	US-11-204-709-21	Sequence 21, Appl
838	108.5	7.0	240	11	US-11-054-515-2025	Sequence 2025, Ap	914	107.5	6.9	241	11	US-11-204-709-22	Sequence 22, Appl
839	108.5	7.0	240	11	US-11-054-515-2029	Sequence 2029, Ap	915	107.5	6.9	241	11	US-11-054-515-1948	Sequence 1948, Ap
840	108.5	7.0	240	11	US-11-054-515-2044	Sequence 2044, Ap	916	107.5	6.9	241	11	US-11-266-444-1948	Sequence 1948, Ap
841	108.5	7.0	240	11	US-11-054-515-2048	Sequence 2048, Ap	917	107.5	6.9	247	11	US-11-266-444-1034	Sequence 1034, Ap
842	108.5	7.0	240	11	US-11-054-515-2105	Sequence 2105, Ap	918	107.5	6.9	259	11	US-11-266-444-1262	Sequence 1262, Ap
843	108.5	7.0	240	11	US-11-266-444-2007	Sequence 2007, Ap	919	107.5	6.9	259	11	US-11-016-503-16	Sequence 16, Appl
844	108.5	7.0	240	11	US-11-266-444-2016	Sequence 2016, Ap	920	107.5	6.9	253	11	US-11-089-803-6	Sequence 6, Appl1
845	108.5	7.0	240	11	US-11-266-444-2025	Sequence 2025, Ap	921	107.5	6.9	253	11	US-11-149-738-2	Sequence 2, Appl1
846	108.5	7.0	240	11	US-11-266-444-2029	Sequence 2029, Ap	922	107.5	6.9	259	11	US-11-149-738-2	Sequence 2, Appl1
847	108.5	7.0	240	11	US-11-266-444-2044	Sequence 2044, Ap	923	107.5	6.9	259	11	US-11-155-269-2	Sequence 2, Appl1
848	108.5	7.0	240	11	US-11-266-444-2048	Sequence 2048, Ap	924	107.5	6.9	458	11	US-11-266-444-1761	Sequence 1761, Ap
849	108.5	7.0	245	11	US-11-266-444-2105	Sequence 2105, Ap	925	107.5	6.9	458	11	US-11-266-444-1761	Sequence 1761, Ap
850	108.5	7.0	245	11	US-11-266-444-1436	Sequence 1436, Ap	926	107.5	6.9	458	11	US-11-266-444-1582	Sequence 1582, Ap
851	108.5	7.0	247	11	US-11-266-444-1436	Sequence 1436, Ap	927	107.5	6.9	458	11	US-11-266-444-1582	Sequence 1582, Ap
852	108.5	7.0	247	11	US-11-054-515-999	Sequence 999, App	928	107.5	6.9	458	11	US-11-266-444-1582	Sequence 1582, Ap
853	108.5	7.0	248	9	US-11-266-444-999	Sequence 999, App	929	107.5	6.9	458	11	US-11-266-444-1582	Sequence 1582, Ap
854	108.5	7.0	248	9	US-10-923-327-15	Sequence 15, Appl	930	107.5	6.9	458	11	US-11-266-444-1582	Sequence 1582, Ap
855	108.5	7.0	249	11	US-11-054-515-919	Sequence 919, App	931	107.5	6.9	463	11	US-11-054-515-1158	Sequence 1158, Ap
856	108.5	7.0	249	11	US-11-054-515-1305	Sequence 1305, Ap	932	106.5	6.9	237	11	US-11-054-515-2110	Sequence 2110, Ap
857	108.5	7.0	249	11	US-11-054-515-1904	Sequence 1904, Ap	933	106.5	6.9	237	11	US-11-266-444-2110	Sequence 2110, Ap
858	108.5	7.0	249	11	US-11-266-444-1305	Sequence 1305, Ap	934	106.5	6.9	242	11	US-11-054-515-1761	Sequence 1761, Ap
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860	108.5	7.0	259	11	US-11-266-444-1304	Sequence 1304, Ap	936	106.5	6.9	244	11	US-11-266-444-1761	Sequence 1761, Ap
861	108.5	7.0	259	11	US-11-054-515-864	Sequence 864, App	937	106.5	6.9	244	11	US-11-266-444-1582	Sequence 1582, Ap
862	108.5	7.0	259	11	US-11-054-515-864	Sequence 864, App	938	106.5	6.9	247	11	US-11-266-444-1582	Sequence 1582, Ap
863	108.5	7.0	438	11	US-11-186-442-10	Sequence 10, Appl	939	106.5	6.9	247	11	US-11-266-444-1582	Sequence 1582, Ap
864	108.5	7.0	438	11	US-11-197-038-34	Sequence 34, Appl	940	106.5	6.9	248	11	US-11-266-444-1582	Sequence 1582, Ap
865	108.5	7.0	438	11	US-11-197-644-34	Sequence 34, Appl	941	106.5	6.9	248	11	US-11-266-444-1582	Sequence 1582, Ap
866	108.5	7.0	439	11	US-11-197-644-33	Sequence 33, Appl	942	106.5	6.9	250	11	US-11-266-444-1582	Sequence 1582, Ap
867	108.5	7.0	439	11	US-11-197-644-33	Sequence 33, Appl	943	106.5	6.9	250	11	US-11-266-444-1582	Sequence 1582, Ap
868	108.5	7.0	439	11	US-11-197-644-33	Sequence 33, Appl	944	106.5	6.9	250	11	US-11-266-444-1582	Sequence 1582, Ap
869	108.5	7.0	439	11	US-11-197-644-33	Sequence 33, Appl	945	106.5	6.9	254	11	US-11-266-444-1582	Sequence 1582, Ap
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871	108.5	7.0	439	11	US-11-197-644-33	Sequence 33, Appl	947	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
872	108.5	7.0	247	11	US-11-113-424-76	Sequence 76, Appl	948	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
873	108.5	7.0	247	11	US-11-266-444-1193	Sequence 1193, Ap	949	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
874	108.5	7.0	247	11	US-11-266-444-1193	Sequence 1193, Ap	950	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
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884	108.5	7.0	248	11	US-11-266-444-1193	Sequence 1193, Ap	960	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
885	108.5	7.0	248	11	US-11-266-444-1193	Sequence 1193, Ap	961	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
886	108.5	7.0	248	11	US-11-266-444-1193	Sequence 1193, Ap	962	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap
887	108.5	7.0	248	11	US-11-266-444-1193	Sequence 1193, Ap	963	106.5	6.9	255	11	US-11-266-444-1582	Sequence 1582, Ap

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965	106	6.9	247	11	US-11-266-444-1707	Sequence 1707, Ap	1038	105	6.8	255	11	US-11-266-444-866	Sequence 866, App
966	106	6.9	249	11	US-11-054-515-2085	Sequence 2085, Ap	1039	105	6.8	259	11	US-11-054-515-1043	Sequence 1043, Ap
967	106	6.9	249	11	US-11-266-444-2085	Sequence 2085, Ap	1040	105	6.8	259	11	US-11-266-444-1043	Sequence 1043, Ap
968	106	6.9	251	11	US-11-259-232-27	Sequence 27, App	1041	105	6.8	302	11	US-11-264-096-2151	Sequence 2151, Ap
969	106	6.9	253	11	US-11-054-515-860	Sequence 860, App	1042	105	6.8	310	11	US-11-217-999-11	Sequence 11, App
970	106	6.9	253	11	US-11-266-444-860	Sequence 860, App	1043	105	6.8	317	11	US-11-217-999-9	Sequence 9, App
971	106	6.9	259	11	US-11-054-515-1277	Sequence 1277, Ap	1044	105	6.8	317	11	US-11-217-999-30	Sequence 30, App
972	106	6.9	259	11	US-11-266-444-1277	Sequence 1277, Ap	1045	105	6.8	340	10	US-11-180-855-3	Sequence 3, App
973	106	6.9	298	11	US-11-085-812-4	Sequence 4, App	1046	105	6.8	340	10	US-11-180-855-3	Sequence 3, App
974	106	6.9	309	9	US-10-453-372-778	Sequence 778, App	1047	105	6.8	464	9	US-10-453-372-772	Sequence 774, App
975	106	6.9	330	11	US-11-085-812-2	Sequence 2, App	1048	104.5	6.8	243	11	US-11-054-515-1935	Sequence 1935, Ap
976	106	6.9	434	11	US-11-204-709-24	Sequence 24, App	1049	104.5	6.8	243	11	US-11-054-515-2051	Sequence 2051, Ap
977	106	6.9	435	11	US-11-204-709-19	Sequence 19, App	1050	104.5	6.8	243	11	US-11-266-444-1935	Sequence 1935, Ap
978	106	6.9	446	11	US-11-102-621-119	Sequence 119, App	1051	104.5	6.8	243	11	US-11-266-444-2051	Sequence 2051, Ap
979	106	6.9	446	11	US-11-102-621-120	Sequence 120, App	1052	104.5	6.8	244	11	US-11-054-515-1524	Sequence 1524, Ap
980	106	6.9	446	11	US-11-102-621-121	Sequence 121, App	1053	104.5	6.8	244	11	US-11-266-444-1524	Sequence 1524, Ap
981	106	6.9	446	11	US-11-102-621-132	Sequence 122, App	1054	104.5	6.8	248	11	US-11-054-515-1237	Sequence 1237, Ap
982	106	6.9	446	11	US-11-102-621-123	Sequence 123, App	1055	104.5	6.8	248	11	US-11-054-515-1717	Sequence 1717, Ap
983	106	6.9	483	11	US-11-299-182-16	Sequence 16, App	1056	104.5	6.8	248	11	US-11-054-515-2071	Sequence 2071, Ap
984	106	6.9	525	11	US-11-236-198-13	Sequence 13, App	1057	104.5	6.8	248	11	US-11-266-444-1237	Sequence 1237, Ap
985	106	6.9	1298	11	US-11-076-427A-12	Sequence 12, App	1058	104.5	6.8	248	11	US-11-266-444-1717	Sequence 1717, Ap
986	106	6.9	1298	11	US-11-075-047A-6	Sequence 6, App	1059	104.5	6.8	248	11	US-11-266-444-2071	Sequence 2071, Ap
987	106	6.9	1362	11	US-11-043-693-33	Sequence 33, App	1060	104.5	6.8	251	11	US-11-054-515-903	Sequence 903, App
988	106	6.9	1363	11	US-11-043-693-32	Sequence 32, App	1061	104.5	6.8	251	11	US-11-054-515-1147	Sequence 1147, Ap
989	106	6.9	1363	11	US-11-076-427A-10	Sequence 10, App	1062	104.5	6.8	251	11	US-11-266-444-903	Sequence 903, App
990	106	6.9	1363	11	US-11-075-047A-121	Sequence 121, App	1063	104.5	6.8	251	11	US-11-266-444-1147	Sequence 1147, Ap
991	106	6.9	1368	11	US-11-043-693-34	Sequence 34, App	1064	104.5	6.8	255	11	US-11-054-515-1914	Sequence 1914, Ap
992	105.5	6.8	239	10	US-11-211-917-64	Sequence 64, App	1065	104.5	6.8	321	11	US-11-266-444-1914	Sequence 1914, Ap
993	105.5	6.8	240	11	US-11-022-040-8	Sequence 8, App	1066	104.5	6.8	321	11	US-11-186-422-8	Sequence 8, App
994	105.5	6.8	244	11	US-11-054-515-1845	Sequence 1845, Ap	1067	104.5	6.8	354	11	US-11-128-900-100	Sequence 100, App
995	105.5	6.8	244	11	US-11-054-515-2069	Sequence 2069, Ap	1068	104.5	6.8	551	11	US-11-000-463-346	Sequence 346, App
996	105.5	6.8	244	11	US-11-266-444-1845	Sequence 1845, Ap	1069	104.5	6.8	681	11	US-11-096-566A-5501	Sequence 2501, App
997	105.5	6.8	244	11	US-11-266-444-2069	Sequence 2069, Ap	1070	104	6.7	249	11	US-11-056-825-8	Sequence 8, App
998	105.5	6.8	247	11	US-11-054-515-1998	Sequence 1998, Ap	1071	104	6.7	249	11	US-11-054-515-1030	Sequence 1030, App
999	105.5	6.8	247	11	US-11-266-444-1998	Sequence 1998, Ap	1072	104	6.7	249	11	US-11-056-825-4	Sequence 4, App
1000	105.5	6.8	248	11	US-11-054-515-848	Sequence 848, App	1073	104	6.7	251	11	US-11-266-444-1030	Sequence 1030, App
1001	105.5	6.8	248	11	US-11-054-515-1675	Sequence 1675, Ap	1074	104	6.7	251	11	US-11-054-515-6	Sequence 6, App
1002	105.5	6.8	248	11	US-11-266-444-1675	Sequence 1675, Ap	1075	104	6.7	251	11	US-11-266-444-6	Sequence 6, App
1003	105.5	6.8	248	11	US-11-266-444-1675	Sequence 1675, Ap	1076	104	6.7	251	11	US-11-266-444-1231	Sequence 1231, App
1004	105.5	6.8	251	11	US-11-054-515-1127	Sequence 1127, Ap	1077	104	6.7	253	11	US-11-266-444-1231	Sequence 1231, Ap
1005	105.5	6.8	251	11	US-11-266-444-1127	Sequence 1127, Ap	1078	104	6.7	253	11	US-11-259-223-55	Sequence 55, App
1006	105.5	6.8	252	11	US-11-054-515-1852	Sequence 1852, Ap	1079	104	6.7	256	11	US-11-054-515-2119	Sequence 2119, Ap
1007	105.5	6.8	252	11	US-11-266-444-1852	Sequence 1852, Ap	1080	104	6.7	256	11	US-11-266-444-2119	Sequence 2119, Ap
1008	105.5	6.8	254	11	US-11-054-515-1045	Sequence 1045, Ap	1081	104	6.7	257	11	US-11-054-515-1256	Sequence 1256, Ap
1009	105.5	6.8	254	11	US-11-054-515-1469	Sequence 1469, Ap	1082	104	6.7	257	11	US-11-266-444-1256	Sequence 1256, Ap
1010	105.5	6.8	254	11	US-11-054-515-1846	Sequence 1846, Ap	1083	104	6.7	257	11	US-11-266-444-1846	Sequence 1846, Ap
1011	105.5	6.8	254	11	US-11-266-444-1045	Sequence 1045, Ap	1084	104	6.7	259	11	US-11-054-515-1025	Sequence 1025, Ap
1012	105.5	6.8	254	11	US-11-266-444-1469	Sequence 1469, Ap	1085	104	6.7	259	11	US-11-266-444-1025	Sequence 1025, Ap
1013	105.5	6.8	254	11	US-11-266-444-1846	Sequence 1846, Ap	1086	104	6.7	259	11	US-11-266-444-1846	Sequence 1846, Ap
1014	105.5	6.8	256	11	US-11-054-515-1285	Sequence 1285, Ap	1087	104	6.7	311	11	US-11-266-444-1270	Sequence 1270, App
1015	105.5	6.8	256	11	US-11-266-444-1285	Sequence 1285, Ap	1088	104	6.7	311	11	US-11-000-463-829	Sequence 829, App
1016	105.5	6.8	274	8	US-10-505-928-115	Sequence 115, App	1089	104	6.7	346	11	US-11-050-857-554	Sequence 554, App
1017	105.5	6.8	274	11	US-11-192-123-19	Sequence 19, App	1090	104	6.7	346	11	US-11-051-720-1384	Sequence 1384, Ap
1018	105.5	6.8	458	11	US-11-016-503-12	Sequence 12, App	1091	104	6.7	1215	8	US-10-505-928-75	Sequence 75, App
1019	105.5	6.8	458	11	US-11-089-803-2	Sequence 2, App	1092	103.5	6.7	213	10	US-11-254-182-54	Sequence 54, App
1020	105.5	6.8	458	11	US-11-218-234-2	Sequence 2, App	1093	103.5	6.7	222	9	US-10-453-372-844	Sequence 844, App
1021	105.5	6.8	458	11	US-11-204-709-6	Sequence 6, App	1094	103.5	6.7	238	9	US-10-496-284-19	Sequence 19, App
1022	105.5	6.8	544	11	US-11-079-463-7763	Sequence 7763, Ap	1095	103.5	6.7	239	10	US-11-211-917-16	Sequence 16, App
1023	105	6.8	228	9	US-10-496-284-15	Sequence 15, App	1096	103.5	6.7	239	10	US-11-211-917-80	Sequence 80, App
1024	105	6.8	228	11	US-11-204-709-20	Sequence 20, App	1097	103.5	6.7	239	10	US-11-211-917-102	Sequence 102, App
1025	105	6.8	245	11	US-11-054-515-1550	Sequence 1550, Ap	1098	103.5	6.7	243	9	US-10-016-686-1	Sequence 1, App
1026	105	6.8	245	11	US-11-266-444-1550	Sequence 1550, Ap	1099	103.5	6.7	243	11	US-11-054-515-1969	Sequence 1969, Ap
1027	105	6.8	247	11	US-11-054-515-1443	Sequence 1443, Ap	1100	103.5	6.7	243	11	US-11-266-444-1969	Sequence 1969, Ap
1028	105	6.8	247	11	US-11-054-515-1711	Sequence 1711, Ap	1101	103.5	6.7	244	11	US-11-054-515-1124	Sequence 1124, Ap
1029	105	6.8	247	11	US-11-266-444-1443	Sequence 1443, Ap	1102	103.5	6.7	244	11	US-11-266-444-1124	Sequence 1124, Ap
1030	105	6.8	247	11	US-11-266-444-1711	Sequence 1711, Ap	1103	103.5	6.7	245	9	US-10-115-609-2	Sequence 2, App
1031	105	6.8	248	11	US-11-054-515-1982	Sequence 1982, Ap	1104	103.5	6.7	245	11	US-11-054-515-1896	Sequence 1896, Ap
1032	105	6.8	248	11	US-11-266-444-1982	Sequence 1982, Ap	1105	103.5	6.7	245	11	US-11-266-444-1896	Sequence 1896, Ap
1033	105	6.8	249	11	US-11-054-515-1986	Sequence 1986, Ap	1106	103.5	6.7	247	11	US-11-054-515-2092	Sequence 2092, Ap
1034	105	6.8	249	11	US-11-054-515-2092	Sequence 2092, Ap	1107	103.5	6.7	247	11	US-11-266-444-2092	Sequence 2092, Ap
1035	105	6.8	249	11	US-11-266-444-1986	Sequence 1986, Ap	1108	103.5	6.7	248	11	US-11-054-515-1267	Sequence 1267, Ap
1036	105	6.8	249	11	US-11-266-444-2093	Sequence 2093, Ap	1109	103.5	6.7	248	11	US-11-266-444-1267	Sequence 1267, Ap

1110	103.5	6.7	250	11	US-11-054-515-1017	Sequence 1017, Ap	1183	102.5	6.6	250	11	US-11-266-444-851	Sequence 851, App
1111	103.5	6.7	250	11	US-11-054-515-11074	Sequence 1174, Ap	1184	102.5	6.6	250	11	US-11-266-444-899	Sequence 899, App
1112	103.5	6.7	250	11	US-11-266-444-1017	Sequence 1017, Ap	1185	102.5	6.6	250	11	US-11-266-444-1977	Sequence 1977, Ap
1113	103.5	6.7	250	11	US-11-266-444-1174	Sequence 1174, Ap	1186	102.5	6.6	251	11	US-11-054-515-1141	Sequence 1141, Ap
1114	103.5	6.7	252	11	US-11-054-515-1557	Sequence 1557, Ap	1187	102.5	6.6	251	11	US-11-054-515-1149	Sequence 1149, Ap
1115	103.5	6.7	252	11	US-11-054-515-1646	Sequence 1646, Ap	1188	102.5	6.6	251	11	US-11-266-444-1141	Sequence 1141, Ap
1116	103.5	6.7	252	11	US-11-054-515-1698	Sequence 1698, Ap	1189	102.5	6.6	251	11	US-11-266-444-1149	Sequence 1149, Ap
1117	103.5	6.7	252	11	US-11-266-444-1557	Sequence 1557, Ap	1190	102.5	6.6	252	11	US-11-054-515-1495	Sequence 1495, Ap
1118	103.5	6.7	252	11	US-11-266-444-1566	Sequence 1566, Ap	1191	102.5	6.6	252	11	US-11-054-515-1518	Sequence 1518, Ap
1119	103.5	6.7	252	11	US-11-266-444-1698	Sequence 1698, Ap	1192	102.5	6.6	252	11	US-11-266-444-1495	Sequence 1495, Ap
1120	103.5	6.7	254	11	US-11-054-515-1866	Sequence 1866, Ap	1193	102.5	6.6	252	11	US-11-266-444-1518	Sequence 1518, Ap
1121	103.5	6.7	254	11	US-11-266-444-1866	Sequence 1866, Ap	1194	102.5	6.6	258	11	US-11-201-825-25	Sequence 25, App1
1122	103.5	6.7	255	11	US-11-054-515-1603	Sequence 1603, Ap	1195	102.5	6.6	260	11	US-11-054-515-1282	Sequence 1282, Ap
1123	103.5	6.7	255	11	US-11-266-444-1603	Sequence 1603, Ap	1196	102.5	6.6	260	11	US-11-266-444-1282	Sequence 1282, Ap
1124	103.5	6.7	291	11	US-11-217-995-10	Sequence 10, App1	1197	102.5	6.6	447	10	US-11-221-902-84	Sequence 84, App1
1125	103.5	6.7	334	11	US-11-113-424-80	Sequence 80, App1	1198	102	6.6	235	9	US-10-453-372-784	Sequence 784, App
1126	103.5	6.7	416	9	US-10-453-372-1028	Sequence 1028, Ap	1199	102	6.6	241	11	US-11-054-515-1303	Sequence 1303, Ap
1127	103.5	6.7	431	11	US-11-198-819-14	Sequence 14, App1	1200	102	6.6	241	11	US-11-266-444-1303	Sequence 1303, Ap
1128	103.5	6.7	431	11	US-11-198-819-20	Sequence 20, App1	1201	102	6.6	250	11	US-11-054-515-1461	Sequence 1461, Ap
1129	103.5	6.7	448	9	US-10-453-372-1024	Sequence 1024, Ap	1202	102	6.6	250	11	US-11-266-444-1461	Sequence 1461, Ap
1130	103.5	6.7	451	9	US-10-453-372-1024	Sequence 1024, Ap	1203	102	6.6	251	11	US-11-054-515-871	Sequence 871, App
1131	103.5	6.7	454	9	US-10-453-372-1022	Sequence 1022, Ap	1204	102	6.6	251	11	US-11-054-515-1806	Sequence 1806, Ap
1132	103.5	6.7	456	9	US-10-453-372-1026	Sequence 1026, Ap	1205	102	6.6	251	11	US-11-266-444-871	Sequence 871, App
1133	103.5	6.7	469	9	US-10-453-372-344	Sequence 344, App	1206	102	6.6	251	11	US-11-266-444-1806	Sequence 1806, Ap
1134	103.5	6.7	471	11	US-11-106-820-25	Sequence 25, App1	1207	102	6.6	252	11	US-11-054-515-1223	Sequence 1223, Ap
1135	103.5	6.7	471	11	US-11-106-820-22	Sequence 22, App1	1208	102	6.6	252	11	US-11-266-444-1223	Sequence 1223, Ap
1136	103.5	6.7	471	11	US-11-190-364-22	Sequence 22, App1	1209	102	6.6	253	11	US-11-054-515-1235	Sequence 1235, Ap
1137	103.5	6.7	471	11	US-11-190-364-23	Sequence 23, App1	1210	102	6.6	253	11	US-11-266-444-1235	Sequence 1235, Ap
1138	103.5	6.7	471	11	US-11-147-780-22	Sequence 22, App1	1211	102	6.6	255	11	US-11-054-515-1281	Sequence 1281, Ap
1139	103.5	6.7	471	11	US-11-147-780-23	Sequence 23, App1	1212	102	6.6	255	11	US-11-266-444-1281	Sequence 1281, Ap
1140	103.5	6.7	488	9	US-10-453-372-1020	Sequence 1020, Ap	1213	102	6.6	257	11	US-11-054-515-1868	Sequence 1868, Ap
1141	103.5	6.7	488	9	US-10-016-686-3	Sequence 3, App1	1214	102	6.6	257	11	US-11-266-444-1868	Sequence 1868, Ap
1142	103.5	6.7	503	9	US-10-453-372-1038	Sequence 1038, Ap	1215	102	6.6	259	11	US-11-054-515-1032	Sequence 1032, Ap
1143	103.5	6.7	527	11	US-11-113-424-81	Sequence 81, App1	1216	102	6.6	458	9	US-11-266-444-1032	Sequence 1032, Ap
1144	103.5	6.7	597	9	US-10-884-730-381	Sequence 381, App	1217	102	6.6	458	9	US-10-453-372-786	Sequence 786, App
1145	103.5	6.7	598	11	US-11-299-182-10	Sequence 10, App1	1218	102	6.6	551	11	US-11-022-289-8	Sequence 8, App1
1146	103.5	6.7	615	11	US-11-198-819-16	Sequence 16, App1	1219	102	6.6	1337	9	US-10-501-035-312	Sequence 312, App
1147	103.5	6.7	615	11	US-11-198-819-18	Sequence 18, App1	1220	101.5	6.6	237	11	US-11-054-515-1906	Sequence 1906, Ap
1148	103	6.7	238	11	US-11-052-554A-38	Sequence 38, App1	1221	101.5	6.6	237	11	US-11-266-444-1906	Sequence 1906, Ap
1149	103	6.7	245	11	US-11-054-515-1591	Sequence 1291, Ap	1222	101.5	6.6	239	11	US-11-054-515-2034	Sequence 2034, Ap
1150	103	6.7	245	11	US-11-054-515-1547	Sequence 1547, Ap	1223	101.5	6.6	240	11	US-11-266-444-2034	Sequence 2034, Ap
1151	103	6.7	245	11	US-11-266-444-1291	Sequence 1291, Ap	1224	101.5	6.6	248	11	US-11-022-040-4	Sequence 4, App1
1152	103	6.7	245	11	US-11-266-444-1547	Sequence 1547, Ap	1225	101.5	6.6	248	11	US-11-054-515-980	Sequence 980, App
1153	103	6.7	249	11	US-11-054-515-1312	Sequence 1312, Ap	1226	101.5	6.6	248	11	US-11-054-515-1246	Sequence 1246, Ap
1154	103	6.7	249	11	US-11-054-515-1971	Sequence 1971, Ap	1227	101.5	6.6	248	11	US-11-054-515-1705	Sequence 1705, Ap
1155	103	6.7	249	11	US-11-266-444-1312	Sequence 1312, Ap	1228	101.5	6.6	248	11	US-11-054-515-1733	Sequence 1733, Ap
1156	103	6.7	249	11	US-11-266-444-1971	Sequence 1971, Ap	1229	101.5	6.6	248	11	US-11-054-515-1737	Sequence 1737, Ap
1157	103	6.7	251	11	US-11-054-515-1551	Sequence 1551, Ap	1230	101.5	6.6	248	11	US-11-054-515-1755	Sequence 1755, Ap
1158	103	6.7	251	11	US-11-266-444-1551	Sequence 1551, Ap	1231	101.5	6.6	248	11	US-11-054-515-1823	Sequence 1823, Ap
1159	103	6.7	253	11	US-11-054-515-1349	Sequence 1349, Ap	1232	101.5	6.6	248	11	US-11-054-515-1879	Sequence 1879, Ap
1160	103	6.7	284	9	US-10-453-372-790	Sequence 790, App	1233	101.5	6.6	248	11	US-11-266-444-980	Sequence 980, App
1161	103	6.7	290	9	US-10-453-372-776	Sequence 776, App1	1234	101.5	6.6	248	11	US-11-266-444-1246	Sequence 1246, Ap
1162	102.5	6.6	239	10	US-11-211-917-56	Sequence 56, App1	1240	101.5	6.6	248	11	US-11-266-444-1705	Sequence 1705, Ap
1163	102.5	6.6	242	11	US-11-054-515-1742	Sequence 1742, Ap	1241	101.5	6.6	248	11	US-11-266-444-1719	Sequence 1719, Ap
1164	102.5	6.6	242	11	US-11-266-444-1742	Sequence 1742, Ap	1242	101.5	6.6	248	11	US-11-266-444-1733	Sequence 1733, Ap
1165	102.5	6.6	246	11	US-11-054-515-1638	Sequence 1638, Ap	1243	101.5	6.6	248	11	US-11-266-444-1737	Sequence 1737, Ap
1166	102.5	6.6	246	11	US-11-054-515-1638	Sequence 1638, Ap	1244	101.5	6.6	248	11	US-11-266-444-1737	Sequence 1737, Ap
1167	102.5	6.6	246	11	US-11-054-515-2068	Sequence 2068, Ap	1245	101.5	6.6	248	11	US-11-266-444-1735	Sequence 1735, Ap
1168	102.5	6.6	246	11	US-11-266-444-1638	Sequence 1638, Ap	1246	101.5	6.6	248	11	US-11-266-444-1873	Sequence 1873, Ap
1169	102.5	6.6	246	11	US-11-266-444-2068	Sequence 2068, Ap	1247	101.5	6.6	248	11	US-11-266-444-1879	Sequence 1879, Ap
1170	102.5	6.6	247	11	US-11-054-515-1400	Sequence 1400, Ap	1248	101.5	6.6	250	11	US-11-054-515-1222	Sequence 1222, Ap
1171	102.5	6.6	247	11	US-11-054-515-1933	Sequence 1933, Ap	1249	101.5	6.6	250	11	US-11-266-444-1222	Sequence 1222, Ap
1172	102.5	6.6	247	11	US-11-266-444-1400	Sequence 1400, Ap	1250	101.5	6.6	251	11	US-11-054-515-890	Sequence 890, App
1173	102.5	6.6	247	11	US-11-266-444-1933	Sequence 1933, Ap	1251	101.5	6.6	251	11	US-11-054-515-894	Sequence 894, App
1174	102.5	6.6	248	11	US-11-054-515-1581	Sequence 1581, Ap	1252	101.5	6.6	251	11	US-11-054-515-910	Sequence 910, App
1175	102.5	6.6	248	11	US-11-054-515-1581	Sequence 1581, Ap	1253	101.5	6.6	251	11	US-11-054-515-1126	Sequence 1126, App
1176	102.5	6.6	248	11	US-11-054-515-1771	Sequence 1771, Ap	1254	101.5	6.6	251	11	US-11-054-515-1157	Sequence 1157, Ap
1177	102.5	6.6	248	11	US-11-266-444-1181	Sequence 1181, Ap	1255	101.5	6.6	251	11	US-11-266-444-890	Sequence 890, App
1178	102.5	6.6	248	11	US-11-266-444-1588	Sequence 1588, Ap	1256	101.5	6.6	251	11	US-11-266-444-894	Sequence 894, App
1179	102.5	6.6	248	11	US-11-266-444-1771	Sequence 1771, Ap	1257	101.5	6.6	251	11	US-11-266-444-894	Sequence 894, App
1180	102.5	6.6	250	11	US-11-054-515-851	Sequence 851, App	1258	101.5	6.6	251	11	US-11-266-444-1126	Sequence 1126, App
1181	102.5	6.6	250	11	US-11-054-515-899	Sequence 899, App	1259	101.5	6.6	251	11	US-11-266-444-1126	Sequence 1126, App
1182	102.5	6.6	250	11	US-11-054-515-1977	Sequence 1977, Ap	1260	101.5	6.6	251	11	US-11-266-444-1157	Sequence 1157, Ap

1261	101.5	6.6	251	11	US-11-266-444-1542	Sequence 1542, Ap	1334	100.5	6.5	237	11	US-11-054-515-2017	Sequence 2017, Ap
1262	101.5	6.6	253	11	US-11-054-515-1509	Sequence 1509, Ap	1335	100.5	6.5	237	11	US-11-054-515-2019	Sequence 2019, Ap
1263	101.5	6.6	253	11	US-11-266-444-1509	Sequence 1509, Ap	1336	100.5	6.5	237	11	US-11-054-515-2020	Sequence 2020, Ap
1264	101.5	6.6	258	11	US-11-054-515-1038	Sequence 1038, Ap	1337	100.5	6.5	237	11	US-11-054-515-2027	Sequence 2027, Ap
1265	101.5	6.6	258	11	US-11-054-515-1042	Sequence 1042, Ap	1338	100.5	6.5	237	11	US-11-054-515-2028	Sequence 2028, Ap
1266	101.5	6.6	258	11	US-11-266-444-1038	Sequence 1038, Ap	1339	100.5	6.5	237	11	US-11-054-515-2040	Sequence 2040, Ap
1267	101.5	6.6	258	11	US-11-266-444-1042	Sequence 1042, Ap	1340	100.5	6.5	237	11	US-11-054-515-2043	Sequence 2043, Ap
1268	101.5	6.6	278	11	US-11-192-123-2	Sequence 2, Ap	1341	100.5	6.5	237	11	US-11-054-515-2104	Sequence 2104, Ap
1269	101.5	6.6	313	11	US-11-000-463-427	Sequence 427, Ap	1342	100.5	6.5	237	11	US-11-054-515-2114	Sequence 2114, Ap
1270	101.5	6.6	453	10	US-11-254-182-44	Sequence 44, Ap	1343	100.5	6.5	237	11	US-11-054-515-2118	Sequence 2118, Ap
1271	101.5	6.6	453	10	US-11-208-422-23	Sequence 23, Ap	1344	100.5	6.5	237	11	US-11-266-444-2003	Sequence 2003, Ap
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1277	101.5	6.6	495	11	US-11-264-096-302	Sequence 302, Ap	1350	100.5	6.5	237	11	US-11-266-444-2028	Sequence 2028, Ap
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